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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Score
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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Match Length
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Gapop 10.0 , Gapext 0.5
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2351
1 MESISMMGSEKSLSETCLEN.....ALVLESIVILDLLQLCRYED 454
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  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Q8nft 2 mus musculu
Q8c5f0 mus musculu
Q9p91 rattus morv
Q8c159 mus musculu
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Q7z389 homo sapien
Q8new6 homo sapien
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## ALIGNMENTS

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	1 MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS 60	Query Match 97.4%; Score 2290; DB 4; Length 490; Best Local Similarity 99.8%; Pred. No. 4.1e-176; Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Pfam; PF03807; F420 oxidored; 1. SEQUENCE 490 AA; 56027 MW; D1971A84880F7E51 CRC64;	d_F420.		Chem. 2	<pre>specific six-trans-membrane protein that is overexpressed in prostate cancer.":</pre>	tion of STAMP1, a highly F		MEDLINE=22229309; PubMed=12095985; Korkmaz C.G., Loda M., Hager G.L.,	rostate;	SEQUENCE FROM N.A.	[1]		Bükaryota; Metazoa; Chordata; Clahtara; Vertebrata; Homo. Mammalia: Firtheria: Primates: Catarrhini: Hominidae; Homo.	Charleston Charleston Vottobtester	2003 (TrEMBLrel.	(TrEMBLrel. 23, Last	(TrEMBLrel. 23, Created)	ORTITE? DESIGNABLE DRT. 490 AA.	ET 1

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Best Local Similarity 99.8
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01-OCT-2002 (TremBI
01-JUN-2003 (TremBI
Six-transmembrane 6
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Porkka K.P., Helenius M.A., Visakorpi T.;
Porka K.P., Helenius M.A., Visakorpi I.;
Postate Cancer.";
SIBAP2, down-regulated in androgen-independent prostate cancer.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

SIBAP2, AA455138; AAN04080.1; -.

Genew, HGNC:17885; STEAP2.
Go; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001618; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420_oxidored; I.
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SEQUENCE 490
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Mammalia; Eutheria;
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Epithelial antigen of prostate 2.
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0; Mismatches 1;
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STRAIN=(57BL/6J; TISSUE=Head;
STRAIN=(22354683; PubMed=12466851;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium Research Group Phase I & II Tea
the RIKEN Genome Exploration Research Group Phase I & II Tea
(6),770 full-length cDNAs.";
Nature 420:563-573(2002).
REMBL; AK052981; BAC35230.1;
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Weakly similar to tumor 3

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Nature 420:563-573(2002)
EMBL; AK078769; BAC37383.1;
MGD; MGI:1915678; Tsap6.
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MEDLINE=22354683; PubMed=12466851;
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Pred. No. 8.4e-98;
1; Mismatches 100
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Sciurognathi; Muridae; Murinae; Mus.
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Q99P41;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRALNE-Dunning, TISSUE-Prostatic carcinoma;
Lu V., Rinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBank/DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Dunning; TISSUE=Prostatic
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Mammalia; Eutheria; Rodentia;
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                                        GIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEBY
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  GVLALGMLSLLAVTSIPSIANSLNWKEFSFVQSTLGFVALMLSTMHTLTYGWTRAFEENH
                                                                                                 QIGLLSFFFAMLHALYSFCLPLRRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEIYLSL
                                                                                                                                             QLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISF
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he EMBL/GenBank/DDBJ
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; Pred. No. 1.2e-97;
81; Mismatches 100;
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Sciurognathi; Muridae;
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ da
EMBL; BC03/7435; AAH37435.1; -.
MGD; MGI:1915678; TBap6.
GC; GC:0006118; P:electron transport; IEA.
INDEPTO; IPR004455; MADPOXIED F420.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54749 MW; 9A08D99C90CF83F4
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01-MAR-2003 (TrEMBLrel. 23, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Similar to RIKEN cDNA 1010001D01 gene.
TSAP6 OR 1010001D01RIK.
Mus musculus (Mouse)
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STRAIN=CZECH II;
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81; Mismatches 100;
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Sciurognathi; Muridae;
                        PRT;
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24,

Created)

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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                                                   Q924Z1;
01-DEC-2001
01-DEC-2001
01-JUN-2003
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GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred_F420.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 526 AA; 58530 MW; 6306CD717E25200A CRC64;
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"The p53-inducible TSAP6 gene product regulates apoptosis cycle and interacts with Nix and the Mytl kinase.";
Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DSMZ ACC331; TISSUE=Bone marrow; MEDLINE=25506415; PubMed=12606722; Passer B.J., Nancy-Portebois V., Amzallag Roborel de Climens A., Fiucci G., Bouvard Morchoisne S.P., Crible V., Lespagnol A.,
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01-OCT-2003
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Mammalia; Eutheria;
 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                              Dudulin 2.
TSAP6 OR 1010001D01RIK.
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Rodentia;
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Sciurognathi; Muridae;
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Serru V., Lamblin D., Lenoir C., Manivet
Kellermann O., Loric S.;
"Molecular cloning and expression of mou
submitted (APR-2001) to the EMBL/GenBank
EMBL; AY029565; AAK50539.1; -
MGD; MGI:1915678; Tsap6.
MGD; MGI:1915678; Tsap6.
GO; GO:0006118; P:electron transport; IE
InterPro; IPR004455; NADPoxred_F420.
Pfam; PF03807; F420 oxidored; 1.
SEQUENCE 514 AA; 57268 MW; 339886C28
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Q86SP6(01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to dudulin 2 (TSAP6).
Homo sapiens (Human).
Homo sapiens (Human).
The Metazoa; Chordata; Craniata; Vertebra
                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Kidney;
Strausberg R.;
Submitted (JAN-2003)
[2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22506415; PubMed=12606722;
MEDLINE=22506415; Portebois V., A
Passer B.J., Nancy-Portebois V., A
Passer B.J., Climens A., Fiucci G.,
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; Pred. No. 8.3e-97;
81; Mismatches 100;
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"The p53-inducible TSAP6 gene product regulates apoptosis and "the p53-inducible TSAP6 gene product regulates apoptosis and rycle and interacts with Nix and the Mytl kinase.";

T cycle and interacts with Nix and the Mytl kinase.";

Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).

R EMBL; BC042150; AAH42150.1; -.

R EMBL; AY214461; AAO38238.1; -.

R GO; GO:0006118; P:electron transport; IEA.

R GO; GO:0006118; P:electron transport; IEA.

R InterPro; IPR003006; Ig_MHC.

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R PROSITE; P800290; IG_MHC; 1.

R PROSITE; P800290; IG_MHC; 1.
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Eukaryota; Metazoa; Ci
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
SEQUENCE FROM N.A.

TISSUB-Human colon endothel primary cell cultu Bloecker H., Boecher M., Mewes H.W., Weil B., Fobo G., Han M., Wiemann S.;

Submitted (UUN-2003) to the EMBL/GenBank/DDBJ EMBL; BX538047; CAD97986.1; -.

Hypothetical protein.

SEQUENCE 498 AA; 55593 MW; 69DD23D5A00C2D6
                                                                                                                                                                                                                                                                  Q7Z389; PRELIMINARY; PRT; 498 AA. Q7Z389; Q1-CCT-2003 (TrEMBLrel. 25, Created) 01-CCT-2003 (TrEMBLrel. 25, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein DKFZp686H07150.

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Best Local Similarity
Matches 242; Conser
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Q9NVB5;
01-OCT-2000
01-OCT-2000
01-JUN-2003
                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
SECUENCE FROM N.A.
SETU V., Manivet P., Lenoir C., Eschwege P.,
Vaubourdolle M., Kellermann O., Loric S.;
"Dudulin 2, a new tumor antigen expressed in v
Submitted (APR-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su Isogai T., Ota T., Hayashi K., Sugano S., Aotsuka S., Yoshikawa Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;

"NEDO human cDNA sequencing project";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2000 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ10829 (Dudulin 2)
Hymothesical protein FLJ10829 (Dudulin 2)
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                             EMBL; AK001691; BAA91839.1; -.
EMBL; AY029585; AAK50538.1; -.
EMBL; AY029585; AAK50538.1; -.
EMBL; AY029585; AAK50538.1; -.
EMBL; AY029585; AAK50538.1; -.
InterPro; IPR003006; IG MHC;
InterPro; IPR004455; NADPoxxed F420.
Pfam; PF03807; F420 oxidored; I.
PROSITE; P$030990; IG MHC; 1.
  Hypothetical
SEQUENCE 4
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Pred. No. 4.4e-94;
B2; Mismatches 108;
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Best Local S
Matches 241
                              QBNEW6;
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01-OCT-2002
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                     (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                 PRELIMINARY;
(Human)
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                     222,
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Pred. No. 7.5e-94;
33; Mismatches 108;
                   Created)
Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.

Lu Y. Beheshti B., Squire J.A., Yang X.J.;

Lu Y. Beheshti B., Squire J.A., Yang X.J.;

Lu Y. Beheshti B., Squire J.A., Yang X.J.;

"Characterization of a novel apoptosis-inducing ge:

"Characterization of a novel apoptosis-inducing ge:

"Characterization of a novel apoptosis-inducing ge:

inhibits prosect to the EMBL/GenBank/DDBJ data

EMBL; AY082673; AAM45136.1; -.

GO; GO;0006118; P:electron transport; IEA.

R GO; GO;0006118; P:electron transport; IEA.

R GO; GO;0006118; P:electron transport; IEA.

R InterPro; IPR003006; IB JWEC.

R InterPro; IPR003006; IB JWEC.

R InterPro; IPR004455; NADPoxred F420.

R InterPro; IPR004455; NADPoxred; I.

JR PROSITE; PS00290; IG_MHC; 1.

PFam; PF03807; P420 oxidored; I.

PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity
Matches 240; Conserv
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Eukaryota; Metazoa;
Mammalia; Eutheria;
    63
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                                                                                                                                                                    SISWMGSPKSTSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRJIRCGYHVVIGSRN
PKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSN--NM
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                                                                                                                                                                                                                                                                      Conservative
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Primates;
                                                                                                                                                                                                                                                                                                  53.3%;
                                                                                                                                                                                                                                                                      83;
                                                                                                                                                                                                                                                                  Score 1252.5; DB 4;
Pred. No. 1.6e-92;
3; Mismatches 108;
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                                                                                             -EAPKVS---ILGSGDFARSLATRLVGSGFKVVVGSRN
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Best Local S
Matches 239
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Steiner M.S., Allay J.A., Wang C.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ date EMBL; AF238844; AAL78206.1; -.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR003006; Ig MHC.

InterPro; IPR003006; Ig MHC.

InterPro; IPR004455; NADPoxred F420.

Pfam; PF03807; F420 oxidored; I.

PROSITE; PS00307; F420 oxidored; I.
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Q8TF03;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor suppressor pHyde. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                        RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
                                                                                                                                                                                                                                                                        SLHLVDSDSSLAK--VPD-----BAPKVS--ILGSGDFARSLATRLVGSGFKVVVGSRN
                                                                                                                                                                                                                                                                                                                  SISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRN 62
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             HALAMGEMEVDMGSLASAWEVEAMPLRLLEAWKVETLLALGLEVCEYAYNEVRDVLQEYV
                                                     LARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATEFFLYSFVRDVIHPYA 240
                                                                                               EHLQHRESNAEYLASLFFTCTVVKAFNVISAWTLQAGFRDGNGQVF1CGDQFEAKRAVSE
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Catarrhini; Hominidae;
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5.8e-92;
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Query Match
Best Local Similarity
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI TaxID=9606;
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Q8TDP3;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR004455; NADPoxred F420.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
PROSITE; PS00290; IG MHC; 1.
SEQUENCE 456 AA; 50430 MW; C5F70
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Wang C., Allay J.A., Steiner M.S.;

"Second human member of pHyde family, Human pHyde II.";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AF262322; AAM08128.1; -.

GO; GO:0006118; P:electron transport; IEA.
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                                                                                                                                                           EEYYRFYTPPNFVLALVLPSIVIL 444
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                    ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQ 395
                                                                     HRKQIGLLSFFCAALHALYSFCLPLRRAHRYDLVNLAVKQVLANKSHLW-VEEVWRMEIY
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LSLGVLALGTLSLLAVTSLPSIANSLNWREFSFVQ
                                                                                                 CRKQLGLLSFFFAMVHVAYSLCLFMRRSERYLFLMMAYQQVHANIENSWNEEEVWRIEMY
                                                                                                                                                                                                              HALAMGEMPVDMGSLASAWEVEAMPLRLLPAWKVPTLLALGLEVCFYAYNFVRDVLQPYV
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                                                                                                                                        QESQNKFFKLPVSVVNTTLPCVAYVLLSLVYLPGVLAAALQLRRGTKYQRFPDWLDHWLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.7%; Score 1074.5; DB
52.9%; Pred. No. 3.2e-78;
tive 75; Mismatches 98
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Last annotation update)
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STRAIN=C57BL/63; TISSUE=Aorta, and Vein;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase 1 & II
"Analysis of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Search completed: April 16, 2004, 12:40:39 Job time: 49 secs

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                         p32212 macaca ; p32212 macaca; p3211us ; q9cn97 gastlus ; q12473 sacchar; q12473 sacchar; q12473 sacchar; p23345 homo sa; p49059 sus sccheri; p31122 escheri; p31124 sacchar; p315743 homo sa; p19901 y genom; p19901 y genom;
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MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

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Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

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putative F420-dependent NADP r
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"Complete genome sequence of jannaschii."; jannaschii."; Science 273:1058-1073(1996).
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Methanocaldococcaceae; NCBI_TaxID=2190;
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Pfam; PF03807; F420 oxidored; 1.
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Hypothetical protein; Oxidoreductase; NADP; Complete p
SEQUENCE 223 AA; 24068 MW; 2370BBD6F5BBD3D9 CRC64;
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STRAIN-Delta H;

MEDIINE-98037514; PubMed=9371463;

MEDIINE-98037514; Dubcette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Smith D.R., Doucette-Stamm L.A., Deloughery C., Gilbert K., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Spadafora R., Pashowski J., Church G.M., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum deltaH; functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155 (1997).
                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria;
Methanobacteriaceae; Methanothermobacter
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20-dependent NADP reductase (EC 1...
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RESULTATION RESULT
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Matches 49
                                                                                                                                                                                                                                                                                                                                                            Macaca fascicularis (Crab
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Primal
Cercopithecinae; Macaca.
NCBI TaxID=9541;
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01-OCT-1993
28-FEB-2003
Follicle sti
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MEDLINE-94071854; PubMed=7504463;

Gromoil J., Dankbar B., Sharma R.S., Nieschlag E.;

"Molecular cloning of the testicular follicle stimulating horr

receptor of the non human primate Macaca fascicularis and

identification of multiple transcripts in the testis.";

Biochem. Biophys. Res. Commun. 196:1066-1072(1993).

-!- FUNCTION: Receptor for follicle stimulating hormone. The of this receptor is mediated by G proteins which activate adenylate cyclase.
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InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420_oxidored; 1.
TIGREAMS; TIGR00301; TIGR0301; 1.
Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
Hypothetical protein; Oxidoreductase; NADP; Complete proteome.
SEQUENCE 232 AA; 24539 MW; A1CE60ABC8474296 CRC64;
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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993 (Rel. 27, Last sequence update)
903 (Rel. 41, Last annotation update)
stimulating hormone receptor precursor
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Chordata; Craniata; Ve
Primates; Catarrhini;
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Pred. No. 0.02
12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             pROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
pROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm_1; Pfam; PF00560; LRR; 3. Pfam; PF01462; LRRNT;
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InterPro; IPR001611;
InterPro; IPR000372;
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SIMILARITY: (
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70013; LRRNT; ;
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Contains 6 leucine-rich (LRR) repeats.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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Bacteria; Proteobacteria;
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(Rel. 41, Last sequence update)
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Follicle stimulating hormone receptor precursor
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STRAIN-White leghorn;

MEDININE-97057887; PubMed=8902217;

You S., Bridgham J.T., Foster D.N., Johnson A.L.;

Ed. FINCTION: Receptor for follicle stimulating hormone of this receptor is mediated by G proteins which accounts receptor is mediated by G proteins which acco
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and forentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata;
                                                                                                                 EMBL; D87871; BAA13487.1;
EMBL; U51097; AAC60030.1;
HSSP; P23945; 1XUN.
InterPro; IPR000276; GPCR
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SUBCELIULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupl
FSH/LSH/TSH subfamily.
SIMILARITY: Contains 7 leucine-rich (LRR) repeats.
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InterPro; IPR001611;
InterPro; IPR000372;
Pfam; PF00001; 7tm\_1

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                                                                                 ROQVIELARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRD
                                                                                                DVQDNIHİRTIERNIFMGLSS---ESVİLR----------LNKNGIQE
                                                                                                            DVSNNMRINOYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQA 174
                                                                                                                                                       I PKGAFTGLHDLEKIEI SQNDALEI I EGNVFSSL
KQLG---
                                                      VIHPYARNOOSDFYKIPIEIVNKTLPIVAITLLSLVYLAGL---------
             KQDLGEQTGKRKHRRSAAEDYISHYGTRFGPVENEFDYGLCNEVVDFVCSPKPDAFNPCE
                                          FİKKLRARSTYKLKKLP--DVNKFRSLIEANFTYPSHCCAFTNRKTQNTEFYPICSMSPA
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N-LINKED (GLCNAC.

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N-LINKED (GLCNAC.
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K-> T (II
N-> S (II
N-> L (II
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (
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4 (IN REF. 2).
7 (IN REF. 2).
6 (IN REF. 2).
5 (IN REF. 2).
6 (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                  Indels 238;
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(POTENTIAL)
(POTENTIAL)
                            -PPWLETWLOCK
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                            302
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) FKED 1....

Q12473;

1 Q12473;

2 Q12473;

1 15-DEC-1998 (Rel. 37, Created)

T 15-DEC-1998 (Rel. 37, Last sequence update)

T 10-CCT-2003 (Rel. 42, Last annotation update)

Ferric reductase transmembrane component 6 precursor

DE (Ferric-chelate reductase 6).

GN FRE6 OR YLL051C OR L0593.

OS Saccharomyces cerevisiae (Baker's yeast).

OS Saccharomyces Saccharomycotan; Saccharomycotane; Saccharomycotane; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Saccharomycefales; Sac
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XX MEDIINE-97313267; PubMed-916987;
XX MEDIINE-97313267; PubMed-916987;
XX MEDIINE-97313267; PubMed-916987;
XX MEDIINE-97313267; PubMed-916987;
XX Dohnston M., Hillier L., Riles L., Albermann K., Duesterhoeft A.,
XX Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
XX Entian K.-D., Floeth M., Goffeau A., Heine K., Koetter P.,
XX Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
XX Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
XX Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
XX Mueller-Auer S., Nentwich U., Obermaier B., Finke M., Rose M.,
XX Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
XX Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
XX Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
XX Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.,
"The mucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
XX Nature 387.87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEAST
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                                                      EMBL; Z47973; CAA88006.1; -.
EMBL; Z73156; CAA97503.1; -.
PIR; S50969; S50969.
GermOnline; 142046; -.
SGD; S0003974; FRE6.
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
STRAIN=S288c / AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).
-!- COFACTOR: FAD (Probable).
-!- SUBCELULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the FRE / CYBB family.
NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
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                                                            REDUCTASE TRANSMEMBRANE COMPONENT
                                                                                                                                             Transmembrane;
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RESULT 8
FRE7_YEAST STANDARD; PRT; 629 AA.
ID FRE7_YEAST STANDARD; PRT; 629 AA.
AC Q12333;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ferric reductase transmembrane component 7 (E
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Matches 72
SEQUENCE FROM N.A.
STRAIN=5388C / FY1579;
MEDLINE=96132030; PubMed=8553699;
Casamayor A., Aldea M., Casas C., H
Lafuente M.J., Gancedo C., Arino J.
"DNA sequence analysis of a 13 kbp
Chromosome XV containing seven new
Yeast 11:1281-1288(1995).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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IF HUMAN STANDARD; PRT; 69:
PSHR HUMAN STANDARD; PRT; 69:
P23945; Q16225;
01-WAR-1992 (Rel. 21, Created)
01-UN-1994 (Rel. 29, Last sequence updi
15-WAR-2004 (Rel. 43, Last annotation updi
Prollicle stimulating hormone receptor porceptor).
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EMBL; Z74894; CAA99174.1; -.
PIR; S60385; S60385
GermOnline; 143574; -.
SGD; S0005512; FRE7:
InterPro; IPR002916; Ferric_reduct.
Pfam; PF01794; Ferric_reduct; 1.
Oxidoreductase; Electron transport; Ti
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Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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SUBJECTLULAR LOCATION: Integral membrane protein SIMILARITY: Belongs to the FRE / CYBB family.
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57; Conservative
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Cargill M.,
Shaw N., Lar
Friedland L.
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Kowalski
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                                                                                                                                                                                                                                                   VARIANTS ALA-307; ARG-524 AND SER-680.
MEDLINE=99318093; PubMed=10391209;
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Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., N
Friedland L., Rolfe A., Warrington J., Lipshutz
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stimulating hormone receptor.";
Biochem. Biophys. Res. Commun. 188:1077-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosenthal J.L., Overton S.A., Wands G.D., Kuze Chappel S.C.;
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Minegish T., Nakamura K., Takakura Y., Ibuki Y., Ig
"Cloning and sequencing of human FSH receptor CDNA.
Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
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                                                                                                                                                                                                      "Characterization of of human genes.";
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ne C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra
., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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Cheng S.V., Nugent N.P., Schweickhardt
L., Overton S.A., Wands G.D., Kuzeja J.
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Genew; HGN MIM; 13643 MIM; 60811 GO; GO:000 GO; GO:000 GO; GO:000 GO; GO:000 GO; GO:000

GO:0016021; GO:0005886; GO:0004963; GO:0007292; GO:0008585; GO:0007186;

C:integral to membrane; TAS.
C:plasma membrane; TAS.
F:follicle stimulating hormone receptor activi
P:female gamete generation; TAS.
P:female gonad development; TAS.
P:G-protein coupled receptor protein signalin.

activity;

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"Ovarian hyperstimulation syndrome due to follicle stimulating hormone receptor.";
New Engl. J. Med. 349:60-766 (2003).
-!- FUNCTION: Receptor for follicle stim of this receptor is mediated by G produced by G pro
                                                                                                                                                     EMBL; M65085; AAA52477.1; -
EMBL; S59900; AAB26480.1; -
EMBL; M56489; AAA52478.1; -
EMBL; X68044; CAA48179.1; -
EMBL; S73199; AAB32071.1; -
EMBL; S73526; AAB32225.1; -
PIR; 157661; QRHUFT.
PDB; 1XUN; 15-MAY-97.
Genew; HGNC:3969; FSHR.
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMSI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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MEDLINE=22812037; PubMed=12930928;
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InterPro; IPR001276; GPCR Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                        ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                                                                                                                                                                                                                                                                                                                                                                       IH-----TIERNSFVGLSFESVILWL----NKNGIQEIHNCA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEDALTKTNIIFVAIHREHYTSLWDLRHLLVG------KILIDVSNNMR 121
                                                                                                                                                                                                                                                                               NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY------
                                                                                                                                                                                                                                                                                                                              ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA
    SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE---
                                            GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVP----RFLMCNLAFAD-----
                                                                                                                                           VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM
                                                                                                                                                                                                                                       RSTYNLKKLP-----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQE
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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N-LINKED (GLCNAC...
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Missing (in isoform &
/FTId=VSP_001953.
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Pred. No. 1.1;
7; Mismatches 148;
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EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
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LRR
LRR
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4 (POTENTIAL
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(POTENTIAL).
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e splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695;
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       ----FSFIQSTL
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유 유 양 명
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15-DEC-1998 (Rel. 37, I
28-FEB-2003 (Rel. 41, I
Follicle stimulating ho
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P49059; C
pfam; pro0001; 7tm_1; 1.

pfam; pro056; LRR; 4.

pfam; pro1462; LRRNT; 1.

pfam; pro1462; LRRNT; 1.

prints; pr00237; GPCRRHODOPSN.

SMART; SM00013; LRRNT; 1.

PROSITE; ps00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; ps50262; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; ps50262; G_PROTEIN_RECEP_F1_2; 1.

phosphorylation; Repeat; Leucine-rich repeat.
                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is no modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     "porcine follicie-stimulating hormone receptor.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for follicle stimulating hormone. The infinite this receptor is mediated by G proteins which activate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE=96011644; PubMed=7590277;
Remy J.J., Lahbib-Mansais Y., Yerle M., Bozon V., Couture L Pajot E., Grebert D., Salesse Y., The porcine follitropin receptor: cDNA cloning, functional expression and chromosomal localization of the gene.";
Gene 163:257-261(1995).
                                                                                                                                                                                                                                                                                                                                                 adenylate cyclase.
-!- SUBCELULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupl
FSH/LSH/TSH subfamily.
-!- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Ovary;
Wang Y.F., Meyer K.B.,
la Barbera A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota, Metazoa;
Mammalia, Eutheria;
                                                                                                                           InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
Dfam. DDCCCO1. Trm 1. 1.
                                                                                                                                                                           EMBL; AF025377; AA
HSSP; P23945; 1XUN
                                                                                                                                                                                         EMBL; L31966; AAA86933.1; -. EMBL; AF025377; AAC24981.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Cetartiodactyla; Suina; Suidae;
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, Last annotation updat
hormone receptor precu
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                                                                                                                                                                                                                                                                                                                                                                                   coupled
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Sus.
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                     signal;
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LPNG-INGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV
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                                                                                                                                                                                                                                                                                               --HEIRIEKANNI-LYIDPDAFQNLPNLRYLLISNTGVKHLPAVHKIQSLQKVLLDIQDN
                                                                                                                                                                                                                                                                                                                                            THHEDALTKINIIFVAIHREHYTSLWDLRHLLVG---
                    RAKSTYNLKKLPSLEXFVTLMEASLTYPSHCCAFANWRRQISDLHPICNKSILRQEVDVM
                                                                 ARNQQSDFYKIP----IEIVNKTL------
                                                                                                                                                      ELARQLNFIPIDLGSLSSARBIBNLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPY
                                                                                                           FNGTQLDELNLSDNDNLEELPNDVFQGASGPVILDISRTRIHSLPSYGLENLKKL
                                                                                                                                                                                                          TVERNSFVGLSFESMILWL----SKNGIRETHNCA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.

N-LINKED (GLCNAC.

N-LINKED (GLCNAC.

N-LINKED (GLCNAC.

S-A (IN REF. 1).

T-S (IN REF. 1).

V-A (IN REF. 1).

V-A (IN REF. 1).

O-A (IN REF. 1).

O-A (IN REF. 1).

S-Y (IN REF. 1).

S-Y (IN REF. 1).

O-A (IN REF. 1).

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O-A (IN REF. 1).
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Pred. No. 1.9;
91; Mismatches
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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FOLLICLE STIMULATING HORMONE RECEPTOR.

EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL) .
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-> H (IN REF. 1).
E9EBEDB29C79C450
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(POTENTIAL)
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RP SEQUENCE FROM N.A.

RC STRAIN=0157:H7 / FIND 0509952;

RX MEDLINE-2115623; PubMed=11258796;

RX HAYSENI T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA HAN C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA HAN C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA HAN C.-G., Ohtsubo E., Nakayama K., Masawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RT "Complete genome sequence of enterohemorrhagic Bscherichia coli

RT "Complete genome comparison with a laboratory strain K-12.";

RI TOTATA and genomic comparison with a laboratory strain K-12.";

RT "OL57:H7 and genomic comparison with a laboratory strain K-12.";

RI DNA Res. 8:11-22(201).

PNA Res. 8:11-22(201).

PNA Res. 8:11-22(201).

CC sugars or sugar metabolites. Transports L-arabinose and to a comparison of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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SOTB OR 22173 OR ECS2135.
Escherichia coli O157.H7.
Bacteria, Proteobacteria; Gammapro
Enterobacteriaceae; Escherichia.
NCBI TaxID=83334;
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P58529;
28-FEB-2003
28-FEB-2003
15-MAR-2004
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Ananthareman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:529-533 (2001).
                                                                                                                                                                (Probable).
SIMILARITY: Belongs (TC 2.A.1.2) family.
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RESULT 12

SOTB ECOLI STANDARD; PRT; 396

ID SOTB ECOLI STANDARD; PRT; 396

AC P31172; P76883; P77333;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence upda

DT 15-MAR-2004 (Rel. 43, Last annotation up

DE Sugar efflux transporter.

GN SOTB OR B1528.
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PROSITE; PS50850; MFS; 1.
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; BAA15210.1; ; BAA15218.1; ; BAA15230.1;

AAC74601.1; -.

(See http://www.isb-sib

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MEDLINE-99369894; PubMed=10438792;
Carole S., Pichoff S., Bouche J.-P.,
"Bscherichia coli gene ydeA encodes a major facilitator pump which
exports L-arabinose and isopropyl-beta-D-thiogalactopyranoside.";
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STRAIN-SB0;

MEDLINE=99194728; PubMed=10094697;

BOST S., Silva F., Belin D.;

BOST S., Silva F. Belin D.;

Transcriptional activation of ydeA, which encodes a member of the

"Transcriptional activation of ydeA, which encodes accumulation

and induction of the Escherichia coli arabinose PBAD promoter.";

J. Bacteriol. 181:2185-2191(1999).
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Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., It
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K. Mori H., Mori T., Motomura K.
Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sai
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wada C., Yanamoto Y., Horiuchi T.;
"A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
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Mau B., Shao Y.;
"The complete genome sequence
Science 277:1453-1474(1997).
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NCBI_TaxID=562;
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MEDLINE=93186717; PubMed=8383113;
Cohen S.P., Haechler H., Levy S.B.;
"Genetic and functional analysis of the resistance (mar) locus in Escherichia J. Bacteriol. 175:1484-1492(1993).
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Blattner F.R., Plunkett G. III, Bloch C.J.
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
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STRAIN=K12 / MG1655;
MEDLINE=97426617; Pu
                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Uentities requires a license agreement (See htt or send an email to license@sisb-sib.ch).
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MEDLINE=99369894;
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SUBCELLULAR LOCATION: Integral
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last sanotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Renal sodium-dependent phosphate transport protein 1 (Sodium/phosphate cotransporter 1) (Na(+)/PI cotransporter 1) (Renal sodium-phosphate transport protein 1) (Renal Na(+)-dependent phosphate cotransporter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, genetic mapping, and expression analysis sodium-dependent phosphate cotransporter."; Am. J. Physiol. 268:F1038-F1045(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95335846; PubMed=7611445;
Chong S.S., Kozak C.A., Liu L., Kristjansson
Bourdeau J.E., Hughes M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007114; MFS.
InterPro; IPR004745; Pi_cotranspt.
TIGRPAMs; TIGR00894; 2A0114euk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X77241; CAA54459.1; -.
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Important for the resorption of phosphate by the kidney May be involved in actively transporting phosphate into cells via Na(+) cotransport in the renal brush border membrane. SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Kidney.
SIMILARITY: Belongs to the sodium/phosphate cotransporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S69915; S69915.
MGI:103209; Slc17a1
                                                                                                                                                                                                                         110 GKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGENVVSAWALQLGPKDA---SRQVY
                                                                                           188
                                                                                                                                                                         167
                                                                                                                                                                                                                                                                   Similarity
--LVYLAGILAAAYQLYYGTKYRREPPWLETWLQCRKQLGLLSEFEAMVHVAXSLCLPMR
                                       SGRQSLP1KAMLKSLPLWÁIILNSFAFIWSNSLLVTYTPTFISTVLHVNVRENGLLSSLP
                                                                                                                                                                      ICSNNIQARQQVIELARQLNFI----PIDLGSLSSAREIENLFLLFTLWRGPVVV----
                                                                                                                                                                                               GLILSSVFFGMVVVQAP----VGYLSGIYPMKRIIGSSLFLSSLMSLLIPPAAQVGAALVI
                                                                                             GFICDLLGWPWVFYIFGIVGCVLSLSWFFLFFDDPXD--HPYMSSSBKDYIISSLMQQAS
                                                                  ---YKIPIEIVNKTLPIVAITLLS--
                                                                                                                                               VCRVLQGIAQGTVSTGQHEIWVKWAPPLERGRLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Symport;
                                                                                                                                                                                                                                                                                                        117
176
199
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;; Sodium transport; T. 99 POTENTIAL.
                                                                                                                                                                                                                                                                   4.48;
18.78;
                                                                                                                                                                                                                                                                                                          51589 MW;
                                                                                                                                                                                                                                                        64;
                                                                                                                      ---AISLATEFELYSEVRDVIHPYARNQQSDF------
                                                                                                                                                                                                                                                     Score 103; DB
Pred. No. 1.5;
64; Mismatches
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                        142;
                                                                                                                                                                                                                                                                                Length 465;
                                                                                                                                                    -MTLSGFVM--GPFIVLLVS
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(POTENTIAL)
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10-OCT-2003
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              InterPro; IPR001135; Oxidored_49kDa.
Pfam; PF00346; compLex1 49Kd; 1.
PROSTITE; P800535; COMPLEX1 49K; 1.
Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast.
SEQUENCE 391 AA; 44913 MW; 9A40AEC68995B25E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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10-0CT-2003 (Rel. 42, Last amnotation update)
NAD[P]H-quinone oxidoreductase chain H, chloroplast (EC 1.6.5.-)
(NAD(P)H dehydrogenase, chain H) (NADH-plastoquinone oxidoreductase
                                                                                                                                                                                                                                                                                                                                        EMBL; AF137379; AAD54891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turmel M., Otis C., Lemieux C.; "The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=NIES-484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99398694; PubMed=10468594;
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                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kDa subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plastoquinol.
SIMILARITY: Belongs to the complex I 49 kDa subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: NAD(P) + plastoquinone = NAD(P)(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN. THE IMMEDIATE TO BE PLASTOQUINONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEPOL
              186 NFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 GLILNQDPEYAWHKISFLMAGINVTCLV---FYFLFAKGEIQDWAK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377 TSIPSVSNALNWREFSFIQSTLGYVALLISTFHVL----IYGWKR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 YLLAYICGILAGQMSDFFLTRK-----IFSIVTVRKLFTTLGSFCPVIFIMCLLYLSYN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
UNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
HAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
DEFLASTOQUINONE: COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF
                                                                                                                                                    85
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                                                 YVTRWDYLATMFTEAITV--------
                                                                                -- SNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQL 185
                                                                                                                                                    KTNIIFVAIHREHYTSLWDLRHLLV---GKILID----
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                                                                                                                 KTDPMIVSM-GPHHPSMHGVLRLIVTLDGENVLDCEPVVGYLHRGMEKIAENRTIVQYLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYSTVIFLTLA----NSTLSFSYCGQLINALDIAPRYYGFLKAVTALIGMFGGLISSTLA 415
                                                                                                                                                                                   Conservative
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                                                 -----NAPERLANIEVPRRA
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STRAIN=16M / ARCC 21456 / Biotype 1;

STRAIN=16M / ARCC 21456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P. H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

Privalla melicancia".
                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sand
28-FBB-2003 (Rel. 41, Last anno
Hypothetical protein BMEII0304.
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Q8YD73;
                                                                                                                                                               HAMAP; MF_01207; -; 1.
InterPro; IPR007916; UPF0191.
                                                                                                                                                                                                      EMBL; AE009669; AAL53546.1; -.
PIR; AG3547; AG3547.
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the B

    -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
    -!- SIMILARITY: Belongs to the UPF0191 family.

                                                                                                                                                                                                                                                                                                                                                                                                                       Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99;443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucellaceae, Brucella.
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                                                                                                                                                                                                    AG3547; AG3547.
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                                                                                                        Pro; IPRUU, .... Pro; IRRUU, ... Pro5252; UPF0191; 1.

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POTENTIAL.
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                                          . protein;
20 39
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85 10;
124 14;
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182C0244743B17FA CRC64;
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Search o	Дъ	γ	рь	γQ	망	γQ	ď	Ş	Query Match Best Local Matches 4
Search completed: April 16, 2004, 12:39:41 Job time : 20 secs	173 M 173	412 I 412	121 RPFÍTIGMISLALLVPLALTSNNWSIRKLGRRWSSLHK-LVÝTÁTAGSAVHFL 172	358 EMYISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVL 411	80 LLRYRRALGLLAFYYALMHFTTYMVLDQGLNLSAIITDIVR- 120	299 -LQCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRI 357	20 LWLLYTAGEVPAVWTEYLGATGQLGADPVKTFBHLLGLWALRFLILTLLLVTPWRDLTGIT 79	267 LSLVYLAGLLAAAYQLYYGTKYRRFPPWLETW	Query Match 4.3%; Score 102; DB 1; Length 220; Best Local Similarity 23.8%; Pred. No. 0.72; Matches 43; Conservative 25; Mismatches 51; Indels 62; Gaps 7;

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Perfect score:
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## ALIGNMENTS

RESULT 1 D95285

conserved hypothetical protein SMa0349 [imported] - Sinorhizobium meliloti (Strain 1021) C.Species: Sinorhizobium meliloti C.Species: Sinorhizobium meliloti (C.Species: Sinorhizobium meliloti C.Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001 C.Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001 C.Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001 C.Date: Poolar A.P.; Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Kalman, S.; Keating, D.H.; Palm, C.; Poolar, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M. Wells, D.H.; Yeh, K.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M.; Wells, D.H.; Yeh, K.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Poolar, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells, M.; Wells,

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Qy 197 SARBIENLPLRLFTLWRGPVVVAISL 222	QY 139 DSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNPIPIDLGSLS 196	Qy 88 IIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFP 138 ::  :      :  :      :  :      :       bb 62 VVILAVFYDSIADIVTQVSDWGGQIVVDASNAIDFPAFKPRDLGGRLSTEIVSELVP 118	Qy 32 TVGVIGSGDFAKSLTIRLIRCGYHVVI-GSRNPKFASEFFPHVVDVTHHEDALTKIN 87   :  :   :  :	Query Match 6.8%; Score 160; DB 2; Length 198; Best Local Similarity 26.7%; Pred. No. 2.1e-05; Matches 55; Conservative 40; Mismatches 83; Indels 28; Gaps 8;	A;Title: The composite genome of the legume symbiont Sinorhizobium mellicl. A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: A;Gene: SMa0349 A;Genome: plasmid	L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K. hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Welle, D.H.; Wong, K.; Yeh, K.	A;Residues: 1-198 < KUR> A;Residues: 1-198 < KUR> A;Cross-references: GB:AB006469; PIDN:AAK64846.1; PID:g14523260; GSPDB:GN00165 A;Experimental source: strain 1021, megaplasmid pSymA A;Experimental source: strain 1021, megaplasmid pSymA R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R;Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R;Galibert, F; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

RESULT 2

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C;Accession: T50571

R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; C; Mol. Microbiol. 21, 77-96, 1996

A;Title: A set of ordered cosmids and a detailed genetic and A;Reference number: Z20556; MUID:97000351; PMID:8843436

A;Accession: T50571

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-239 <RED>

A;Cross-references: EMBL;AL133220; PIDN:CAB61708.1

A;Experimental source: strain A3(2)
C;Genetics: A;Note: SCC75A.08c

C;Superfamily: conserved hypothetical protein MJ1501
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AC2560
C;Accession: AC2560
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigue Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ja;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2560
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A;Genome: plasmid
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Similarity 24.9%; Pred. No. 2.4e-05;
51; Conservative 43; Mismatches 70;
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                                                                                                                        IKDARKVTVGVI-GSGDFAKSLTIRLIRCGYHVVIGSR---NPKFASEFFPHVVDVTHHE
  ETARRSDVVIVAVPWDGHGKTLESLRABLSGKLVVDCVNPLGFDKKGAVALKPEBGŚAAB
                                                                                                                                                                                     6.7%; Score 156.5; DB 2; 27.9%; Fred. No. 5e-05;
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Conserved hypothetical protein AF1209 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Dec 1997 #sequence_revision 05-Dec 1997 #text_change 29-Sep-1999 C;Date: 05-Dec 1997 #sequence_revision 05-Dec 1997 #text_change 29-Sep-1999 C;Accession: H69400 R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dc R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dc R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Fleischmann, J.F.; McDonald, L. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch; A;Reference number: A69250, MUID:98049343; PMID:9389475
A;Accession: H69400
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A; Residues: 1-213 <KLE>
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| 56; Conserv
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                                                                                                     KLÁSVLEESSVVAAYHSIPÄRRFANLGEEFEWDVPİCGDS-GÄKEVVVDLTEKISGLRAL
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DAGGLSNAHLVESLTPLILNVMKR 202
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                                                     DLGSLSSAREIENL-PLRLFTLWR 213
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irkness, E.F.
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C;Accession: D69361
C;Accession: D69361
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodsor R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Oyerbeek, R.; Gcoayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C. Smith, H.O.; Woese, C.R.; Venter, J.C. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Ression: D69361
A;Status; preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Ressidues: 1-212 <KLE> conserved hypothetical protein AF0892 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 29-Sep-1999

A;Cross-references: GB:AE001042; GB:AE000782; C;Superfamily: conserved hypothetical protein NID: g2689365; MJ1501 PIDN:AAB90348.1; PID:g264970

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RESULT 7

D64487

hypothetical protein MJ1501 - Methanococcus jannaschii

C; Species: Methanococcus jannaschii

C; Species: Methanococcus jannaschii

C; Species: Methanococcus jannaschii

C; Species: Methanococcus jannaschii

C; Accession: D64487

R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.M.; Hurst, M.A.

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.

Science 273, 1058-1073, 1996

A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch
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R;Berk, H.; T
FEBS Lett. 43
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A;Experimental source: strain Marburg
C;Superfamily: conserved hypothetical
C;Keywords: oxidoreduction
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FEBS Lett. 438, 124-126, 1998
A;Tittle: F420H2:NADP oxidoreductase from Methanobacterium thermoautotrophicum:
A;Reference number: Z16959; MUID:99037734; PMID:9821972
A;Accession: T10120
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Matches 49
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;Spate: 16.-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
.accession. T10106
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59; Conserv
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29.2%;
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25.4%; Pred. No. 0.0006;
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RESULT A69131

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A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64487
A;Status: preliminary; nucleic acid sequence not shown; translation
A;Molecule type: DNA
A;Residues: 1-223 <BUL>
A;Residues: 1-223 <BUL>
A;Residues: 1-223 <BUL>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Wegenome Res. 11, 731-753, 2001
A;Title: The complete ganome sequence of the lactic acid bacterium A;Reference number: A86625; MJID:21235186; PMID:11337471
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                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005176; PID:g12724621;
A;Experimental source: strain IL1403
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Best Local S
Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: F86826
                                                                                                                                                                                                                                                                                                                                                                   :Genetics:
                                                                                                                                                                                                                                                                               Matches
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 154
                                   190
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46; Conserv
                                                                                                                                                                                                                                                                           Ch 5.1%; Score 121; DB 2; Similarity 22.2%; Pred. No. 0.024; 47; Conservative 33; Mismatches 74
                                                                                                                                                                                                          w
                                                                                                                                                                                                                                                                                                                                                                                                                 1-191 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNVLKESKVVSAFQNVCHAVLEDLDNPVDCDILVCGNDEBAKKVVIDLANQIDGVRAIDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLFPDSLIVKGFNVVSAWALQLGFKDASRQVYIÇSNNIQARQQVIELARQLNFI-PIDL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGDVVILSLPYBYTLSTIKQLKEELKGKIVVSIGVPLATAIGDKPTRLLFPPDGSVÄEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTNIIFVAIHREH-YTSLWDLRHLLVGKILIDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGDQGFGLALRLAK-NNKIIIGSRKKEKAEEAAKKAKEILKQRGIEADIIGLENKDAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDV------THHEDALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSLSSAREIENLPLRLFTLWRGPVVVAISL
                                                                                                  ASLFPDSLIVKGFNVVSAWALQLGPKDASRQ----VYICSNNIQARQQVIELARQLNFIP 189
                                                                                                                                     VVLAVPYVAIAGIIQEYSTD------LQGKIIDITNPVDFTTFDSLLVPSDTSAAALI
                                                                                                                                                                     -----IIFVA, HR. BHYTSLWDLRHLLVGK, ILIDVS, NWRINQYPE------SNABYL 133
                                                                                                                                                                                                          TISIFGKGKMGKAI--
 LDAGSLKRÄRELEAIGFLQITLAASEKISWDG
                               IDLGSLSSAREIENLPLRLFTL-----WRG
                                                                  AKQLPNSMIVKAFN--TTFSDTLATKKVANEHQTTVLLASDSQEAKETTIKALENSGLSL
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21.9%;
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Pred. No. 0.0033;
52; Mismatches 78;
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     185
                                                                                                                                                                                                              --GDNFSSSVNKVNYILSNSSKTELGEI
                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAK05712.1;
                                                                                                                                                                                                                                                                                   74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                          GSPDB:GN00146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus
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A;Cross-references: GB:AE000811; GB:AE000666; NID:g2621287; PIDN:AAB84754.1; PID:g262129
A;Experimental source: strain Delta H
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z14115; MUID:98332717; PMID:9666070
A;Accession: T00121
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-216 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicalre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 Methanobacterium thermoautotrophicum Delta H: funct A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
A; Roccession: A69131
A; Roccession: A69131
A; Status: preliminar; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Leptospira interrogans
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C;Accession: T00121
R;Takahashi, Y; Akase, K.; Hirano, H.; Fukunaga, M.
Gene 215, 37-45, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 215, 37-45, 1998 A_{\rm c} Title: Physical and genetic maps of the Leptospira interrogans serovar icterohaemorrha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein 8 - Leptospira interrogans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL;AB010203; NID:g2780763; PIDN:BAA24368.1; PID:g2780765; Experimental source: strain Ictero No.1; substrain icterohaemorrhagiae
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Local Similarity 23.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AEYLASLF---PDSLIVKGENVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81
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                                                                          66 VLCSKGSVASEVLTLSGIDSLNGKTIIDTTNPISEIPPQNGVLNFFTSYNESLMEKLQKQ 125
                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                       33 VGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHV---VDVTHHEDALTKTNII 89
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                                                                                                                                                                                                                            Q,
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FPDSLIVKGFNVVSAWALQLGP--KDASRQVYICSNNIQARQQVIELARQLNFIPIDLGS 194
                                                                                                                                                     FVAIHREHYTSLWDLRHL--LVGKILIDVSNNMR-----INQYPESNAEYLASL 136
                                                                                                                                                                                                                                IGILGSGIVGQTLANGFLKYGAEVKIGTRDFGKLKDWLAKAGAGASIGSFSEAANFGEII
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 119.5; DB 23.7%; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                  37;
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                                                                                                                                                                                                                                                                                                                                                                                  91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 216;
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; F
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, M.V.; Martins, F.
A;Authors: Martins, E.M.F.; Matskuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.F.
Rodrigues, V.; Rosa, A.J. de N.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasabi
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.R.; Tsuhako, M.H.; Vallada, H.; Van Silvs, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C/Species: Xylella fastidiosa
C/Species: Aylella fastidiosa
C/Jate: 18-Aug-2000 ##equence_revision 20-Aug-2000 #text_change 20-Aug-2000
C/Accession: G82642
Rainonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
Attrice 151-157, 2000
Attrice: The genome sequence of the plant pathogen Xylella fastidiosa.
Attrice: The genome sequence of the plant pathogen Xylella fastidiosa.
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Attrice: The genome sequence of the plant pathogen Xylella fastidiosa.
Attrice: The genome sequence of the plant pathogen Xylella fastidiosa.
C;Accession: AB3182
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
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                                                                                                                                                                                                                        conserved hypothetical protein Atu5183 [imported] - Agrobacterium tumefaciens C_\ellSpecies: Agrobacterium tumefaciens
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C;Species: Xylella fastidiosa
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                                                                                                                                                                                      Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 LSSAREIENLPLRLFTLW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 APKANFVKCFSSVGS-GLMVNPQLKGEKPSMFICGNDDSSKKQIKEILDTFGWDTEDMGK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 IVĠNĹAAAASFQ 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 EFGTVLLLAVPFEALPQVGRDLRSAYRGKIVLDSTNPWGASSADVYREARELGVAQTVVK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 TKTNIIFVAIHREHYTSLW-DLRHLLVGKILIDVSNNWRINQ---YPESN----AEYLAS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 AAPMRIGVIGAGSLGGTVGRLWVKAGHEVMFSSRNPDKLBAMARELEPR-ASVGQPLAAT 88
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46; Conserv
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A;Molecule type: DNA
A;Residues: 1-198 <KUR>
A;Cross-references: GB:
F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology clrR4>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology clrR5>
F;146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology clrR5>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology clrR7>
F;194-218/Domain: transmembrane #status predicted <ff>cff
F;367-387/Domain: transmembrane #status predicted <ff>cff
F;39-421/Domain: transmembrane #status predicted <ff>cff
F;444-465/Domain: transmembrane #status predicted <ff>cff
F;486-508/Domain: transmembrane #status predicted <ff>cff
F;486-508/Domain: transmembrane #status predicted <ff>cff
F;597-597/Domain: transmembrane #status predicted <ff>cff
F;597-597/Domain: transmembrane #status predicted <ff>cff
F;590-630/Domain: transmembrane #status predicted <ff>cff
F;591-199,299,318/Binding site: carbohydrate (Asn) (movalent) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phosphate (Tim) (covalent) (by protein kinase C) #status predicted F;596/Binding site: phospha
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F;18-695/Product: follitropin receptor #status predicted <PFHs
F;19-95/Product: follitropin receptor #status predicted <PFHs
F;71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3 > F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7 > F;121-145/Domain: leucine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Gromoll, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E. Biochem. Biophys. Res. Commun. 196, 1066-1072, 1993
A;Title: Molecular cloning of the testicular follicle stimulating A;Reference number: JN0898; MUID:94071854; PMID:7504463
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A; Title: The Genome of
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A; Residues: 1-695 < GRO>
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;Gene: Atu5183
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Similarity 17.0%;
84; Conservative 7
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                                                                                                                                                                                                                                                                                               ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                       ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                                                                                                         INQYPESNAEYLASLFPDSLIVKGENVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
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                                               VYTLTAITLERWHTITHAMQLDCKVHVRHAASVMVMGWIFAFAAALFPIFGISSYMKVSI
                                                                                                                       WNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE-----
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                      APPRIATEDITOR
                                                                                                                                                                         ----LLSFFFAMVHVA---
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                                                                                              -LCIGIYLLLIASVDIHTKSOYHNYAIDWOTGAGCDAAGFFTVFASELS
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75; Mismatches
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                                                                         VLIYGWKRAFEEEYYRFYTPPNFV-LAL 436
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RESULT 14

S59681 membrane protein YPL012w - yeast (Saccharomyces cerevisiae)

yrobable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)

yrobable membrane protein YPS0132.01

(Species: Saccharomyces cerevisiae

C; Species: Saccharomyces cerevisiae

C; Aperiae: 13-Jan-1996 #sequence revision 01-Mar-1996 #text\_change 19-Apr-2002

C; Accession: S59681, S52519

C; Accession: S59681, S52519

R; Hall, U.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.;

submitted to the EMBL Data Library, August 1995

A; Accession: T128 < HAL
A; Accession: S59681

A; Accession: S59681

A; Accession: S59681

A; Cross-references: EMBL, U33335; NID:g965076; PID:g965081; MIPS:YPL012w

A; Cross-references: EMBL, U33335; NID:g965076; PID:g965081; MIPS:YPL012w

A; Cross-references: EMBL, C48483; NID:g965076; PID:g965081; MIPS:YPL012w

A; Experimental source: strain AB972

C; Generics:
A; Generics:
A; Generics:
A; Generics: SGD:S0005933

A; Cross-references: SGD:S0005933

A; Map position: transmembrane #status predicted <TM1>
F; 125-141/Domain: transmembrane #status predicted <TM3>
F; 220-736/Domain: transmembrane #status predicted <TM3>

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Db 8 GTGDIGAGLALRWATDSDHDIVIGSRDÞEKARETAAAYEDTLADQGVDRKLTGFANEMAA 67

Qy 84 TKTNIIFVAIHREHYTSLW------DLRHLLVGKILIDVSNNWRINQYÞESNAE---YL 133

Bb 68 DRADVVVAVÞAYHYTDVWGAVADRLDADTLVISÞAVGIASGEHGLHYNÞÞSAGSVTALV 127

QY 134 ASLÞÞDSL-IVKGÞNVVSAWALQLGÞKDASRQVICSNNIQARQQVIELARQLNFI-ÞID 191

QY 136 DRADVVVAVÐAYHNILAÐARLADLDTELDADTLVVGNDEGARTRVAELADDITGLRALD 187

DB 128 ADDARÞGVDVVGAFHNILAÐARLADLDTELDADTLVVGNDEGARTRVAELADDITGLRALD 187

QY 192 LGSLSSAREIENLFLIKURR 213

DB 188 AGÞVENAAEVESLTÞLLINLAR 209
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Search completed: April 16, 2004, 12:41:12 Job time : 23 secs

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Result
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Maximum DB seq length: 2000000000
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US-10-455-822-33

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PUBCOMB. pep: *
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## ALIGNMENTS

RESULT 1 US-09-888-257A-10

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Sequence 10, Application US/0988257A
Publication No. US20030060612A1

GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Paul J
APPLICANT: Goddward, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Hillan, Kenneth J
APPLICANT: Hillan, Kenneth J
APPLICANT: Wood, William I
APPLICANT: Wood, William I
APPLICANT: Wood, William I
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APPLICANT: Wood, William I
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APPLICANT: Wood, William I
APPLICANTON WOMBER: US/09/888,257A
CURRENT FILING DATE: 1997-10-28
PRIOR APPLICATION WOMBER: US/09/888,257A
CURRENT APPLICATION WOMBER: US/09/888,257A
PRIOR APPLICATION WOMBER: US/09/888,257A
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION WOMBER: US/09/888,257A
PRIOR PILING DATE: 1998-09-10
PRIOR PILING DATE: 1998-09-10
PRIOR APPLICATION WOMBER: US/09/493-478 NO
PRIOR PILING DATE: 1998-09-10
PRIOR APPLICATION WOMBER: US/09/493-478 NO
PRIOR FILING DATE: 1999-09-09
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PRIOR FILING DATE: 1990-09-09
PRI
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Sequence 3, Application US/10455822
; Sequence 3, Application WIS20040048798A1
; GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Jakobovite, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
FITILE OF INVENTION: Entitled 98P4B6 Useful in Treatment and Determine File Reference: 51158-20016-24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT APPLICATION NUMBER: US/10/455,822
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/0370,387
PRIOR FILING DATE: 2002-04-05
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 10
LENGTH: 454
TYPE: PRT
ORGANISM: Homo Sapien
US-09-888-257A-10
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
NUMBER: OF SQU ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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; ORGANISM: Homo
US-10-455-822-3
RESULT 3
US-10-455-822-7
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Matches 454
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Local Similarity 100.0%; Pred. No. 6.1e-222;
nes 454; Conservative 0; Mismatches 0; Indels 0;
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                                                                                 EBYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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Detection of Cancer

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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
SECTION NO
                                                                                                                                                        Sequence 9, Application US/1045822
Publication No. US20040048798A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
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; TYPE: PRT
; ORGANISM: Homo sapian
US-10-455-822-7
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APPLICANT: Paris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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Pred. No. 6.1e-222;
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US-10-455-822-19
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR PILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo sapian US-10-455-822-9
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Matches
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                       EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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                                                                            ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
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Pred. No. 6.1e-222;
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Sequence 19, Application US/10455822

Publication No. US20040048798A1

(GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Farie, Mary
TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and Detection of PIICE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT APPLICATION NUMBER: No. US20040048798A1 Yet Assigned PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned PRIOR APPLICATION NUMBER: US/03-06-04

PRIOR APPLICATION NUMBER: US/03-06-04

PRIOR APPLICATION NUMBER: US/03-06-04

PRIOR APPLICATION NUMBER: US/03-06-04

PRIOR APPLICATION NUMBER: US/03-06-04

PRIOR FILING DATE: 2002-12-04-05
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Sequence 21, Application US/1045822

Publication No. US20040048798A1

GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: WILLE OF INVENTION: Entitled 98P436 Useful in Treatment and Determine OF INVENTION: Entitled 98P436 Useful in Treatment and Determine APPLICATION NUMBER: US/10/455,822

CURRENT APPLICATION NUMBER: US/00404048798A1 Yet Assigned PRIOR APPLICATION NUMBER: US/0070,387

PRIOR APPLICATION NUMBER: US/070,387

PRIOR APPLICATION NUMBER: US/070,387
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ORGANISM: Homo sapian
US-10-455-822-19
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
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SEQ ID NO 19
LENGTH: 454
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Best Local Similarity
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APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Galita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
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Publication No. US20040048798A1
         TITLE OF INVENTION: Nucleic acids and Corresponding Proteins TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and FILE REFERENCE: 51158-20016.24 CURRENT APPLICATION NUMBER: US/10/455,822 CURRENT FILING DATE: 2003-06-04 PRIOR APPLICATION NUMBER: NO. US2004004879BA1 Yet Assigned PRIOR PILING DATE: 2002-12-20 PRIOR PILING DATE: 2002-13-20 PRIOR PILING DATE: 2002-04-05
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Detection

of Cancer

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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
1 SEQ ID NO 21
1 LENGTH: 454
TYPE: PRT
1 ORGANISM: Homo sapian
US-10-455-822-21
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Matches 454;
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                        EEYYRFYTTPPNFVLALVLPSIVILDLLQLCRYPD
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; PRIOR FILING DATE: 1998-06-01; NUMBER OF SEQ ID NOS: 197; SOFTWARE: FastSEQ for Windows Ve; SEQ ID NO 23; SEQ ID NO 23; LENGTH: 454; TYPE: PRT; ORGANISM: Homo sapian
US-10-455-822-23
                                                                                                                                                                                                                                                                                                                 RESULT 8
US-10-455-822-25
; Sequence 25, App
; Publication No.
                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Agensy, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Fid, Pia M.
APPLICANT: Faris, Mary
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PRIOR FILING DATE: 2001-09-06
PRIOR PPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
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Best Local (
                                                                          APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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Similarity 100.0%; Pred. No. 6.1e-222;
54; Conservative 0; Mismatches 0;
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10. US20040048798A1
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PRIOR FILING DATE: 1998-06-30, PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 25
LENGTH: 454
TYPE: PRT
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RESULT 9
US-10-455-822-31
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PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR PPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR PPLICATION NUMBER: US60/087,520
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                                                                                                      BEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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US-10-455-822-31

(Sequence 31, Application US/10455822

Sequence 31, Application US/1045798A1

(SERIERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Agensys, Inc.

APPLICANT: Agensys, Inc.

APPLICANT: Agensys, Arthur B.

APPLICANT: Galtano, Arthur B.

APPLICANT: Galtano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Faris, Mary

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: 2016-24

PRICE REPERIOR: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT FILING DATE: 2003-06-04

PRICE APPLICATION UNMBER: US/040048798A1 Yet Assigned

PRICE APPLICATION NUMBER: US/0300,387

PRICE APPLICATION NUMBER: US/0300,387
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Sequence 33, Application US/1045822

Sequence 33, Application US/20040048798A1

GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
ITILE OF INVENTION: Entitled 98P4B6 Useful in Treatment and FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned PRIOR APPLICATION NUMBER: US/01/370,387
PRIOR APPLICATION NUMBER: US/03-03-03-04

PRIOR APPLICATION NUMBER: US/03-03-03-04

PRIOR APPLICATION NUMBER: US/03-03-04

PRIOR APPLICATION NUMBER: US/03-03-03-04

PRIOR APPLICATION NUMBER: US/03-03-03-04

PRIOR APPLICATION NUMBER: US/03-03-03-04

PRIOR APPLICATION NUMBER: US/03-03-03-04
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR REFLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
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; ORGANISM: Homo sapian
US-10-455-822-31
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US-10-455-822-33
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 454
TYPE: PRT
GREANISM: Homo sapian
US-10-455-822-33
Sequence 35, Application US/10455822

Publication No. US20040048798A1

GENERAL INFORMATION:

APPLICANT: Regensys, Inc.

APPLICANT: Regensys, Inc.

APPLICANT: Reltano, Arthur B.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Faris, Wary

ITILE OF INVENTION: Mucleic acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and Det.

FILE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT FILLING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR APPLICATION NUMBER: US60/370,387
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Best Local Similarity 100.
Matches 454; Conservative
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Pred. No. 6.1e-222;
; Mismatches 0;
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Detection

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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-30
PRIOR PILING DATE: 1998-06-01
NUMBER: OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapian
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US-10-455-822-37
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                                                                                                                                                                                             APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
TITLE OF INVENTION: Nucleic acids and Corresponding Prote
TITLE OF INVENTION: Entitled 98P486 Useful in Treatment
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigns
PRIOR FILING DATE: 2002-12-20
PRIOR PILING DATE: 2002-13-03
PRIOR FILING DATE: 2002-04-05
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No. US20040048798A1
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APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Uskobovits, Aya
APPLICANT: Uskobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
ITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and
FILE REFERENCE: 51158-20016-24
FILE REFERENT SILING INTE: 2003-06-04
PRIOR APPLICATION NUMBER: US/10/455,822
PRIOR APPLICATION NUMBER: No. US/20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/20040048798A1 Yet Assigned
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; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo s
US-10-455-822-37
RESULT 13
US-10-455-822-39
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-01
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 37
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Best Local Similarity 100.
Matches 454; Conservative
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                                                                                                                 EEYYREYTEPNEVLALVLPSIVILDLLQLCRYPD
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Assigned

f Proteins

Detection of Cancer

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RESULT 14
US-10-455-822-78
; Sequence 78, Applicati
; publication No. US2004
; publication No. US2004
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FREESEQ for Windows Version 4.0
APPLICANT: Ageneys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatmen
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assig
PRIOR APPLICATION NUMBER: US20070,387
PRIOR FILING DATE: 2002-04-05
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LENGTH: 454
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Best Local Similarity 100.0%;
Matches 454; Conservative 0;
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No. US20040048798A1
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Pred. No. 6.1e-222;
; Mismatches 0;
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Sequence 121, Application US/10455822

Publication No. US20040048798A1

Publication No. US20040048798A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Agensys, Inc.

APPLICANT: Ge, Wangmao

APPLICANT: Chalita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Paris, Mary

ITILE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and Determing Proteins

TITLE OF INVENTION: UNUMBER: US/10/455,822

CURRENT APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR FILING DATE: 2002-04-05
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PRIOR FILLING DATE: 2001-09-06
PRIOR PELLING DATE: 2001-06-06
PRIOR PELLING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 198-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR PILLING DATE: 198-06-01
NUMBER OF SEQ ID NOS: 197
SOPTWARE: PASTSEQ FOR WINDOWS Version 4.0
SEQ ID NO 78
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; TYPE: PRT
; ORGANISM: Homo sapian
US-10-455-822-78
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Pred. No. 6.1e-222;
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILLING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapian
US-10-455-822-121
Search completed: April 16, 2004, 12:46:36 Job time: 49 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 LARQLNEIPIDLGSLSSAREIENLPLRLETLWRGPVVVAISLATEFELYSEVRDVIHDYA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 RINOYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
                                                                                                                                        421 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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Title: Perfect :

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70,7, Appl
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101, Appl
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Post-processing: Minimum Match 0%
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2351
1 MESISMMGSPKSLS
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Match
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 2004, 12:38:02 ;
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        US-09-323-873A-8
US-09-083-521-1
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US-09-083-5270A-2
US-09-665-166A-879
US-09-665-1941-17
US-08-487-886-2
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US-08-333-873A-20
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US-09-975-413A-6009
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1065.372 Million cell updates/sec
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US-09-323-873A-8
   RESULT 2 0
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; Sequence 1, Application US/09083521
; Patent No. 6048970
; GENERAL INFORMATION:
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Best Local Similarity
Matches 173; Conserv
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US-09-903-456-45

US-09-903-456-707

US-09-107-52AP-707

US-09-107-52AP-9411

US-09-328-352-5605

US-09-328-352-5605

US-09-328-352-991P-23822

US-09-528-991P-23822

US-09-534-238-281

US-09-134-601C-3105

US-09-134-001C-3105

US-09-134-001C-3105

US-09-134-001C-3105

US-09-134-001C-3105

US-09-138-0318-7503

US-09-118-093B-26

US-09-178-093B-26

US-09-795-927-7
                                                                                                                                                                                                                      Score 901; DB 4; 1
Pred. No. 1.4e-86;
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Gaps

120 365 60 305 Result No.

144.5 144.5 144.5 107.5 107.5 107.5 107.5 107.5 107.1 107.1 109.9 99.9 99.9 97.9 99.9 97.9 94.5

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Sequence 2, Application US/09323873A
Patent No. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 85-055
TELEPAX: (650) 85-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USU2
CURRENT FILLING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM FORMATIBLE
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APPLICANT: Corley, Neil C.

TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              314 MYHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LAVTSIPSVSNALNWREFSFIQSTLGYVÄLLISTFHVLIYGWKRAFBEEYYRFYTPPNFV 120
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATS CANCER
FILE REFERENCE: 210121.427C21
FULE REFERENCE: 210121.427C21
FULE REFERENCE: 2000-10-10
FURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPPE: Dem
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US-09-685-166A-879
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PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 879, Application US/09685166A Patent No. 6630305 GENERAL INFORMATION:
                                                                   Query Match 30.5%; Score 717; DB 4; Length 339; Best Local Similarity 54.9%; Pred. No. 8.5e-67; Matches 130; Conservative 48; Mismatches 59; Indels
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Best Local Similarity
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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208 LFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQSDPYKIPIEIVNKTLPIVAITLL 267
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Carter, Darrick
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Mitcham, Jennifer L.
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ick, Thomas S.
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RESULT 6
US-09-651-941-17
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Patent No. 6355470
GENERAL INFORMATION:
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Patent No. 63291
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Best Local &
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APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
FILE REFERENCE: BC1022 US NA
CURRENT EPLICATION NUMBER: U5/09/651,941
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic File Reference: BC1011 US NA CURRENT APPLICATION NUMBER: US/09/655,270A CURRENT FILING DATE: 2000-09-05 PRIOR APPLICATION NUMBER: 60/120,702 PRIOR APPLICATION NUMBER: 60/120,702 PRIOR APPLICATION NUMBER: 60/120,702 PRIOR APPLICATION NUMBER: 60/120,702 PRIOR APPLICATION NUMBER: 60/150,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-655-270A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 QYPESNAEYLASLFPDSLIVKGFNVVSA---WALQLGPKDASRQVYICSNNIQARQQVIE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 AADNASĀAADCPĪĪLLVVPYDGHRĒLVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 LFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIPILVINKVLPMVSITLL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 VTHHEDALTKTNIIFVAI----HREHYTSLWDLRHLLVGKILI------DVSNNMRIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 IKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPH-------VVD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 60; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsoft Office 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 144.5; DB 4; Length 227;
Liarity 28.0%; Pred. No. 6.4e-07;
Conservative 33; Mismatches 88; Indels 33
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S: 37
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TYPE: PRT
ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-17
        RESULT 8
US-08-487-886-2
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-955-597-17
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Best Local S
Matches 60
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APPLICANT: ROUVIER, PIERRE E

APPLICANT: WALTERS, DANA M

APPLICANT: RAINER, RUSS

TITLE OF INVENTION: Genes Encoding Picric Acid Degradation

FILE REFERENCE: BC1022 US NA

CURRENT APPLICATION NUMBER: US/09/955,597

CURRENT APPLICATION NUMBER: 099-17

PRIOR APPLICATION NUMBER: 60/152,545

PRIOR APPLICATION NUMBER: 60/152,545

PRIOR APPLICATION DATE: 1999-10-03

NUMBER OF SEQ ID NOS: 28

NUMBER OF SEQ ID NOS: 28
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SEQ ID NO 17
LENGTH: 227
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SEQ ID NO 17
LENGTH: 227
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Best Local :
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No. 6461856
                                                                                                               173 LAVAITGRÉGIDGGALRVARQLEFLTAVLINVNR 206
                                                                                                                                                                181 LARQUNFIP-IDLGSLSSAREIENLPLRLFTLWR 213
                                                                                                                                                                                                                116 VEEGSAAEQLRDLVPGATVVAAFHHLSAVNLWEHE-GP--LPEDVLVCGDDRSAKDEVAR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR 206
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                                                                                                                                                                                                                                                                 124 OYPESNAEYLASLFPDSLIVKGFNVVSA---WALQLGPKDASRQVYICSNNIQARQQVIE 180
                                                                                                                                                                                                                                                                                                                          59 AADNASAAADCPIILLVVPYDGHRELVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD 115
                                                                                                                                                                                                                                                                                                                                                                        76 VTHHEDALTKTNIIFVAI----HREHYTSLWDLRHLLVGKILI-----DVSNNMRIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 IKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPH------VVD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AADNASAAADCPIILLVVPYDGHRELVS---ELAPIFAGKLVVSCVNPLGFDKSGAYGLD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 6.1%; Score 144.5; DB 4; Length 227; 1 Similarity 28.0%; Pred. No. 6.4e-07; 60; Conservative 33; Mismatches 88; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 VTHHEDALIKINII FVAI --- HREHYTSLWDLRHLLVGKILI ----- DVSNNMRIN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKSSKIAVVG--GTGPQGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRRAGDGAVVS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKSSKIAVVG--GTGPQGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRRAGDGAVVS 58
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 33; Mismatches

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Patent No. 57444
GENERAL INFORMA
APPLICANT: Y
APPLICANT: 5
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CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,08!
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/2:
TELECOMMUNICATION INFORMATION:
TELEPHAN: (617) 723-1300
TELEPHAN: (617) 723-1300
TELEPAN: (617) 723-1300
TELEPAN: (617) 723-1300
TELEPAN: (617) 723-1300
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APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 5744448een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/487,886
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MEDIUM TYPE: 3.5" di
                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                        NAME/KEY: putative transmembrane region I LOCATION: 350 to 370 IDENTIFICATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled recommendation of the protein-coupled recommendation method: hydrophobic, about
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: transmembrane domain LOCATION: 350 to 613 IDENTIFICATION METHOD: similar:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD: IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                NAME/KEY: putative transmembrane region II LOCATION: 382 to 404 IDENTIFICATION METHOD: similarity to other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: putative amino-terminal extracellular domain LOCATION: 1 to 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109
                                                                   IDENTIFICATION METHOD:
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                    NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PS/2,
putative transmembrane region III 427 to 448
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BM PS/2, model 55 SX
STEM: MS-DOS version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07/670,085
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                                                                                                                                                                                                           similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
                                                              similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
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                                                                   436 LVLPSIVILDLLQL 449
                                                                                                                456 SVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGISSYMKVS
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                                                                                                                                                                                                                                                                                                           361 GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVP-----RFLMCNLAFAD------
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614 to 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity to other G protein-coupled receptor transmembrane regions hydrophobic, about 20-23 amino acids in length
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US-08-482-855-2
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GENERAL INFORMATION:
APPLICANT: Kelton
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670
APPLICATION NUMBER: 15-MAR-1991
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TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28846
REFERENCE/DOCKST NUMBER: U
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MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: 1EM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Massil via Kermit to IBM MS-DOS
CURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,855
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LENGTH: 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 723-1300
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                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: transmembrane domain LOCATION: 350 to 613 IDENTIFICATION METHOD: similari IDENTIFICATION METHOD: protein-
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ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: putative amino-terminal extracellular domain LOCATION: 1 to 349
IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receptor extensive procession of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the complex control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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NAME/KEY: putative transmembrane region II (CCATION: 382 to 404 (CCATION METHOD: similarity to other IDENTIFICATION METHOD: protein-coupled receiptoral formula (Company) (Company) (Company) (Company) (Company) (CCATION METHOD: protein-coupled receiptoral formula (Company) (CCATION METHOD: hydrophobic, about 2)
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)GY: Linear
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similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
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Best Local S
Matches 84
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IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptions. IDENTIFICATION METHOD: hydrophobic, about 20
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          436 LVLPSIVILDLLQL 449
                                                                        456 SVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGISSYMKVS 515
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1 Similarity 17.0%; Pred. No. 0.028;
84; Conservative 77; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                  G-----LLSFFFAMVHVA-------YSLCLPMRRSERYLFLNMAYQQVHANIEN 347
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512 to 533
TION METHOD: similarity to other
TION METHOD: protein-coupled rec
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592 to 613
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557 to 580
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Length 695;

Gaps

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US-08-474-986-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28446
REFERENCE, POCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
LOCATION: 614 to 678
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match. Match. 17.0%; Score 107.5; DB 4; Length 695; Local Similarity 17.0%; Pred. No. 0.028; Length 695; Gaps 64; Conservative 77; Mismatches 148; Indels 185; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density

COMPUTER: IBM PS/2, model 55 SX

OPERATING SYSTEM: MS-DOS version 4.0

SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/670,085
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Uun-1995
CLASSIFICATION: cUnknown>
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:

ADDRESSE: Stephan P. Williams,
ADDRESSE: Exer-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Cheng, Shirley Vui Yen
Nugent, No. 6372711een Patrice
TITLE OF INVENTION: Human Follicle Stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                               182 ARQUNFIPIDLGSISSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 ICLPMDIDSPLSQL 529
                                           247 RSTYNLKKLP-----TLEKLVALMEASLTYPSHCCAFANWRRQISELHPICNKSILRQE 300
                                                                                                                                                                                                                              242 NQQSDFYKIPIEIVNKTL-PIVAITLLSLVY-------
                                                                                                                                                                                                                                                                            190 ---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA 246
                                                                                                                                                                                                                                                                                                                                                                     157 IH-----TIERNSFVGLSFESVILWL---NKNGIQEIHNCA----- 189
361 GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVF-----RFLMCNLAFAD----- 408
                                                                                        301 VDYMTQTRGQRSSLÄEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSPKPDAFNPCEDIM 360
                                                                                                                                                                                                                                                                                                                                                                                                                  122 INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
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                                                                                                                                   ------PPWLETWLQCRKQL 305
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COUNTRY: USA
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APPLICANT: Rene S. Hubert
APPLICANT: Kahan Leong
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TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-30
NUMBER: 05/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER: FOR SEQ ID NOS: 32
SOFTWARB: FastSEQ for Windows Version 4.0
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; Sequence 8165, Application US/09328352
; Patent No. 6562958
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                                                                                                                            ; ORGANISM: Acinetobacter baumannii US-09-328-352-8165
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GATY L. BETCON et al.
APPLICANT: GATY L. BETCON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 8165
LENGTH: 940
TYPE: PRT
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Query Match
4.4%; Score 102.5; DB 4; Length 940;
Best Local Similarity 19.5%; Pred. No. 0.15;
Matches 71; Conservative 74; Mismatches 146; Indels 73
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US-09-316-083-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09316083A Patent No. 6280942
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APPLICANT: The Inst
                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                             SROVYICSNNIOAROOVIELAROLNFIPIDLGSLSSARBIBNLPLRLFTLWRGPVVVAIS
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                                                                                                                                                                                                                                LRHLLVGKILIDVSNNWRINQYPESNAEYLASLF - - PDSLIVKGFNVVSAWALQLGPKDA 161
                                                                                                                                                                                                                                                                NPYFVNAFSINI-----KTNLAKEKI FTNIYNKLYSDYKINQINNHI PYYNYLK
                                                                                                                                                                                                                                                                                                NPKFASEFFPHVVDVTHHEDALTKINI----IFVAIHREHYT-------SLWD 103
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                                                                                          LATFFFLYSFVRDVIHPYARNQQSDFYKIP----IEIVNKTLDIVAITĻLSLVYLAGLLA
DNYDYYYYNKY
                               AAYQLYYGTKY 288
                                                                                                                               -RPSYVIS-QVETRXELIYLIQB----SFDL-SISNVKKVGNRKLKDFKLFTRTTDELMK
                                                               ----FIYYF--DKFLPLHDNKOFNYIKFRFNTFIKSYNWNNRVFGLVLSB--YINNIKI
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452

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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO F
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/00/074,788
PRIOR APPLICATION NUMBER: US/00/04,788
PRIOR APPLICATION NUMBER: US/00/04,190
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21494
LENGTH: 724
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US-09-252-991A-21494
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                                                                                   US-09-252-991A-21494
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SEQ ID NO 3
LENGTH: 476
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Best Local Similarity
Matches 52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21494, Application US/09252991A Patent No. 6551795
Query Match 4.3%; Score 101; DB 4; Length 724; Best Local Similarity 20.5%; Pred. No. 0.14; Matches 72; Conservative 57; Mismatches 105; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/933, CURRENT FILING DATE: 2001-08-20 PRIOR APPLICATION NUMBER: 09/316,083 PRIOR FILING DATE: 1999-05-20 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The Institute of Physical and Chemical Research TITLE OF INVENTION: Endonuclease FILE REFERENCE: PH-651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                         ORGANISM: Pseudomonas aeruginosa
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48; Mismatches
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	565 TDTAIQHSLGLGGKSRPNTRÁLTMLPLIRNVLFATIAVIÁLIVA 608		Дb
	367SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLIS 406		δ
564	516 FVVLFFIEVALRVWGMSLIR-YAEGEGEQISMKVVSFGTTLLVAWLIWIL 564		DЬ
366 6	318 AYSICLEMRRSERYLFINMAYQQVHANIENSWNEBEVWRIEM-YISFGIM 366		δÃ
515	472 VLAVVAMTVIGLIRRRSSRVGAGPRRSAPYIBQLQSFGYTLLHI 515		В
317	TLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRREPEWLETWLQCRKQLGLLSEFFAMVHV 317		δ
471	412 LIRNOPLERRLKRRSLHDLVQLVGSLWFVPVLVLVGISLFATFVSAGDSSSALRRALVCA 471		Db.
257	239 YARNQQETVNK 257		Ş
411	FRPLWLIGSLAALGEVAHDFRLIAGLGEHTSICLSTLANASAALFTALFVMRFRRPIAH- 411	353	ф
238	187 FIPIDL-GSLSSARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHP 238		8
352	3 YLSVVLPDSL-SKTLAMWAYVLVCGTLFSALCVISLSLLSGPHRQRALDILRRQA 352	298	Дb
186	132 YLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186		Ş

Search completed: April 16, 2004, 12:41:47 Job time : 24 secs

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protein search, using

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Aay58195 Aam180937041 Abb37041 Abb37041 Abb31810 Abb22356 Aam70183 Aam77188 Abg51883 Aam75646 Abg39817 Aau04565 Abg52889 Abu60886

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 AAU10220
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Aae02781 Human six
Aau10188 Human ORF
Abg61933 Prostate
Aau76538 Tumour-as
Aau80190 Human pro
Aae28951 Human pro
Aae28951 Human six
Aau10187 Human Six
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Aau10187 Human ORF
Abg12306 Novel hum
Abg020113 Novel hum
Aae02113 Novel hum
Aae021316 Human pro
Aau404548 Human pro
Aau04564 Human Tum
Aab8376 Human Tum
Aab8376 Human Gp
Aau04564 Human Gp
Aau04564 Human Gp
Aau10220 Human Gp
Aau10220 Human Gp
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                                                                                                                                                                                                                                                                                                                                                               Human six transmembrane epithelial antigen of prostate (STEAP)-2
                                                                                                                                                                                                                                                                                  Key
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CC prostate (STEAP)-2 protein. STEAP is a membrane epithelial antigen of the contraremembrane antigens. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is located on chromosome 7q21 and is compared the therapy. Inhibiting the development or progression of a comparison prostate, colon, bladder, lung, ovarian and pancreatic) compressing STEAP or inhibiting growth or killing cells expressing STEAP or comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or comprises the variable domains of the heavy and light comprises the variable domains of the heavy and light comprises the variable domains of the heavy and light comprises the variable domains of the heavy and light comprises the single chain monoclonal comprises the single chain monoclonal antibody that the vector delivers the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal complete the single chain monoclonal antibody is expressed intracellularly. Note: This sequence is stated to listing of the specification. However both the sequences differ at coveral positions
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                                            ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU10188
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New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, comprises prostate-specific or testis-specific nucleic acids.

Claim 1; Fig 4H; 114pp; English

The invention relates to substantially pure prostate-specific or testiscoling controlling them. Also included CC specific polypeptides and the nucleic acids encoding them. Also included CC are vectors and host cells expressing the proteins, a transgenic animal cexpressing the protein, antibodies against the proteins, probes for CC expressing the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that CC modulate the proteint especific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate CC particularly prostate cancer, beaign prostatic hyperplasia, acute CC prostatitis, testicular cancer, cryptorchidism, undescended, retractile, CC ascending or vanished testis. Other proliferative disorders for which the CC cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer. CC The present sequence is prostate specific protein, Six-Transmembrane CC protein of Prostate 1, STMP1, ORF2

Query Match Best Local ( 454; Similarity

Sequence

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Length

454;

밁 5 밁 Matches 61 ۳ RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDPAKSLTIRLIRCGYHVVIGS MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNIM 100.0%; ilarity 100.0%; Conservative 0 0 Score 2351; DB 4 Pred. No. 5e-245; Mismatches 0 0 Indels 0 Gaps 120 120 60 60 0

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08-DEC-2000;
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The present invention relates to methods of detecting a prostate can associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer
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16-MAR-2001;
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The invention relates to an isolated tumour-associated antigenic target CC polypueptide (TAT) (I), specifically TAT138 polypeptides, and the CC polypueleotides (II) encoding them. (II) is useful for diagnosing the CC presence of a tumour in a mammal, where the level of expression of (II) is indicative on the presence of tumour in the mammal from which the test cample was obtained. Antibody to (I) is useful for killing a cancer cell, a colorectal cancer cell, a lung cancer cell, a colorectal cancer cell, a lung cancer cell, a liver cancer cell, a central nervous system (CNS) cancer cell, a colorectal cancer cell, a pancreatic cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a colorectal cancer cell, a cancer cell, a cancer cell, a cancer cell, a colorectal cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, 
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26-SEP-2000; 2000US-0235451F.
01-DEC-2000; 2000WO-US03678.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated tumor-associated antigenic target polypeptides which useful as targets for cancer therapy and diagnosis in mammals.
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/note= "Tyrosine kinase phosphorylation site"
428. .448
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29. .32
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Best Local Simi
Matches 454;
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                                                                                                                                                                                                                                                                        Human PUMPCn protein, PRO23203.
                                                                                                                                                                                                                                                                                                        15-JUL-2002
                                                                                                                                                                                                                                                                                                                                    AAU80190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
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Human; protein upregulated in metastatic prostate cancer; immunogen; PUMPCn; PRO23203; prostate cancer; cytostatic; gene therapy; transge androgen independent prostate cancer; DNA microarray.

Homo

WO200226822-A2

04-APR-2002.

26-SEP-2001; 2001WO-US030290

26-SEP-2000; 2000US-0235451P

(GETH ) GENENTECH INC

Devaux B, Eberhard D, Goddard A, Godowski PJ, Grimaldi JC;

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CC The invention relates to an isolated human protein upregulated in CC identical to prostate cancer (PUMPCH) PRO23203 polypoptide, a sequence 80% CC identical to PRO23203 and the sequence as encoded by CDNA insert of the CC vector deposited as ATCC Deposit No. PTA-2513 (DNA185171-2994) on C2 26/9/2000. Also included are the polymucleotide by CDNA insert of the C2 DNA sequence 80% identical to the polymucleotide and one that C2 DNA185171-2913 (DNA185171-2994) on C2 DNA185171-2913 (DNA185171-2994), a host cell comprising the vector, C2 preparation of PRO23203, a chimeric molecule comprising the vector, C3 preparation of PRO23203, a chimeric molecule comprising PRO23203 fixed to C3 Activation and in a mammal by: (a) contacting a microarray diagnostic with a C3 DNA185171-2994 probe, detecting and diagnosing the presence of prostate C4 cancer in a mammal by: (a) contacting a microarray diagnostic with a C4 contacting a tissue of the mammal with an anti-PRO23203 antibody and C4 contacting a tissue of the mammal with an anti-PRO23203 antibody and C5 contacting a tissue of the presence of prostate cancer in the mammal with an anti-PRO23203 antibody and C5 contacting a tissue of the presence of prostate cancer in the mammal with an anti-PRO23203 antibody and C6 contacting a tissue of the presence of prostate cancer in the mammal cancer in the mammal with an anti-PRO23203 and prostate cancer in the mammal with an anti-PRO23203 and prostate cancer in the mammal cancer in the section of contacting either transgenic animals or knock out animals which in turn cancer in the prostate cancer in the presence of prostate cancer in the presence of prostate cancer in an mammal and screening of therapeutically useful cancer that mammal and for chromosome identification. C6 pro23203 may also be employed as a therapeutic agents and for servening cancer in the effect of the PRO23203 polypoptide consensing the present the effect of the PRO23203 polypoptides. The present call culture or natural sources. The present confidence is the pre
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                                       RNQQSDFYKIBIEIVNKTLBIVAITLLSLVYLAGLLAAAYQLYYGTKYRREPPWLETWLQ
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02-MAR-2000;
30-MAR-2000;
24-AUG-2000;
The invention discloses human nucleic acids encoding tumour-associated antigenic target (TAT) polypeptides, with our without their associated signal peptide. Also disclosed is an antibody that specifically binds the TAT polypeptides, a method for detecting the presence of a tumour is a mammal and a method for killing a cancer cell expressing the TAT polypeptide. The nucleotide sequences are useful in preparing TAT polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The TAT polypeptides by recombinant techniques and in gene therapy therapeutic agents and for detecting the presence, prevention and/or therapeutic agents and for detecting the presence, prevention and/or treatment of a tumour, such as colon, breast or prostate tumour. The TA polypeptides and nucleic acids may also be used diagnostically for ties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour-associated antigenic target 138 (TAT138)
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17-JUN-1998;
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08-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, useful for the manufacture diagnosing or treating tumor in a mammal.
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28-FEB-2001;
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DB; ACD25893.
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herapy; cytostatic; tissue typing; prostate tumour; cancer.
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2000WO-US005841.
2000WO-US008439.
2000WO-US023328.
2000WO-US023328.
2000WO-US025451P.
2000WO-US006520.
2001WO-US006520.
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 Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                 05-NOV-2001; 2001JP-00379298.
25-JAN-2002; 2002US-00350978.
                                                                                                                                                               28-MAR-2002; 2002EP-00007401
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Otsuki T, Wakamatsu A, Sato H, Hio Y, Otsuka K, Nagai K, Irie Otsuka M, Nagahari K, Masuho Y;
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New polynucleotides and polypeptides, useful for developing a diagnomarker or medicines for regulation of their expression and activity, as targets of gene therapy.

The invention discloses a polynucleotide comprising a sequence selected CC from 1970 fully defined nucleotide sequences which encode novel collined; as a polypeptide encoded by the polynucleotide cor its partial peptide, an antibody binding to the polypeptide or peptide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide of the polynucleotide by contacting the polypeptide or peptide or peptide of the polynucleotide by contacting the polypeptide or peptide with the antibody of the encoded protein, and observing the binding CC between the two, a transformant carrying the polynucleotide in an expressible manner and an antisense polynucleotide. The oligonucleotide concerns are useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The polynucleotide and encoded concerns are useful as pharmaceutical agents and many disease-related concerns are useful as proteins, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of genes therapy. The genes are involved in tissue and/or cell cranscription-related proteins, disease-related proteins, curvanscription-related proteins, disease-related proteins and genes cancer, tumours. The colM may be used to regulate the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the sequence data for this patent is not represented in the printed by the European Patent Office.

Sequence 454 AA;

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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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                               EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
                                                                    ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                                     ISFGIMSLGLISLIAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                                                                        CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEBEVWRIEMY
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Pred. No. 1.1e-244;
1; Mismatches 0;
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Best Local Simi
Matches 444;
                                                                                                                                                                                                                                                                                                                             The invention relates to six-transmembrane epithelial antigen of the prostate related protein (STEAPRP) and its corresponding nucleic acid. STEAPRP DNA is used to diagnose and to treat prostate call proliferative disorders, particularly prostate hyperplasia and prostate cancer, and for screening a library of molecules of compounds for specific binding affinity. It is also used in gene therapy. STEAPRP is used to screen a subject sample for antibodies, which specifically binds the protein, and to prepare and purify a protein. The present sequence is human STEAPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New six-transmembrane epithelial antigen of the prostate-related protein and nucleic acids, useful for diagnosing and treating prostate cell proliferative disorders, particularly prostate hyperplasia and prostate
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                                                                                                                                                                                                                                                                                             Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13;
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                                                                                        RINGYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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                                                              LARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
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                                                                                                                                                                                                                                             Conservative
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id. No. 8.4e-239;
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the prostate related!
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The invention relates to a purified human protein comprising a copypeptide having a fully defined transmembrane protein differentially compressed in prostate and lung tumour (TMPL) sequence. The protein is cuseful for detecting expression of the protein in a sample, where the comparison is a sample is lung or prostate tissue sample and the protein is diagnostic of a lung or prostate cancer. The protein is useful to identify an compared with a standard and is diagnostic of a lung or prostate cancer. The protein. The protein is useful for screening several molecules and compounds to identify at least one compared. The protein is useful for protein is useful for protein and purifying a complete of the protein and purifying a copyclonal antibody and for preparing a monoclonal antibody using completed to detect expression of the protein in a lung or prostate cancer. A TMPL specific antibody is useful to detect expression of the protein in a lung or prostate cancer. A TMPL specific antibody is a diagnostic for lung or corostate cancer. A TMPL specific antibody is a diagnostic for lung or protein is useful for diagnosting a prostate cancer and for compounds to incomparifying a protein, for treating a prostate cancer and for the protein is useful for diagnosing, staging, treating or monitoring compounds to the protein is useful for cancer, preferably lung or prostate cancer. The present sequence represents the amino acid sequence of the human constants.
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16-SEP-1999; 99US-0039753.

09-MAR-2001; 2001US-00963896.

26-SEP-2001; 2001US-00963896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transmembrane protein differentially expressed in prostate and luntumors, useful for diagnosing, staging, treating or monitoring progression or treatment of cancer, preferably lung or prostate cancer
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The invention relates to substantially pure prostate-specific or testiscolor specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal captures of the protein, antibodies against the proteins, pubbes for the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that the modulate the proteins or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate compounds that the proteins proteins or prostate compounds that the proteins of the testis or prostate compounds that the proteins of the testis or prostate compounds that the proteins of prostate that the compounds that the protein of prostate cancer, benign proteinic paypeptide are useful compounds that the protein testis or prostate the protein of prostate the protein of protein of the testis or prostate cancer, cancer, interactive disorders for which the conditators may be used include lymphoma, leukaemia, melanoma, ovarian compounds that the protein sequence represents a prostate specific protein, Six-

Transmembrane Protein of Prostate 1, STM;1
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                                                                                                                                                                                                                                       The invention relates to substantially pure prostate-specific or testiscolors specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, brobes for detecting the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that conducte the proteins protein that the protein that the protein that the protein the protein compounds that the dispose, prevent or treat disorders of the testis or prostate are useful to diagnose, prevent or treat disorders of the testis or prostate C particularly prostate cancer, benign prostatic hyperplasia, acute constitis, testicular cancer, captorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the cancer breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic cancer, leukaemia, melanoma, ovarian cancer, breast cancer, pancreatic sepecific protein, Six-Transmembrane concerned the prosent sequence is prostate specific protein, Six-Transmembrane concerned the protein of Prostate 1, STM;1, ORF3
                                                                                                                                        Query Match
Best Local Similarity
Matches 394; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide for the diagnosis, prevention and treatment for prostate and testis disorders, particularly prostate cancer, compr. prostate-specific or testis-specific nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              liver cancer; lung cancer; cytostatic; ORF3.
                                                                                                                                                                                                            Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAAT/) SAATCIOGLU F.
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                          RNPKFASEFFEHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also use in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating useful for generating antibodies against it, detecting or quantitating polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorder, involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 42665; 103pp; English.
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DB; AAS76493.
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medical imaging; diagnostic; genetic disorder.
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Pred. No. 6.7e-204;
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Sequence 1273 AA;

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CC sequences. (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polymucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity Cresponsible for genetic disorders or other traits to assess biodiversity C and to produce other types of data and products dependent on DNA and CC amino acid sequences . ABG00010-ABG30377 represent novel human diagnostic C matern did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences
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S 밁 Ś 뮍 Ş Ş 밁 Ś 뮍 S 밁 S 밁 5 밁 Matches Beat Query Match Local 373 313 241 253 193 133 421 361 301 181 121 390; 61 73 Similarity RINQYPEGNABYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHBEHYTSLWDLRHLLVGKILIDVSNNM RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESISWAGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS CRKQLGLLSFFFAMVHVAYSLCLFMRRSERYLFLNMAYQQVHANIENSWNEBEVWRIEMY RNQQSDFYKIFIBIVNKTLFIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFFFWLETWLQ RNQQSDFYKIPIBIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRPPPWLETWLQ LARQUNFIPIDLGSLSSARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA LARQLNFIPIDLGSLSSARBIENLFLRLFTLWRGFVVVAISLATFFFLYSFVRDVIHFYA MESISMMGSPKSLSETFLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS EEYYRFYTPPNFVLALVLPSIVILDL ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQ 83.9%; milarity 87.4%; Conservative °. Score 1972.5; DB 4 Pred. No. 2.3e-203; 0; Mismatches 1; 463 446 **QSTLGYVALLISTFHVLIYGWKRAFE** 4. Indels Length 55, 180 192 120 132 60 360 312 240 420 372 300 252 437 411

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                                                The present sequence is an alternative version of human six transmembrane epithelial antigen of the prostate (STEAP) 2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP agene is concerned on chromosome 7021 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting a vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP in a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering a comprises administering to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, comprises the cancer cells and the encoded single chain monoclonal squence to the cancer cells and the encoded single chain monoclonal comprises that being shown as SEQ ID No.8 (AAE02781) in figure 9A-9C of the specification. However the present sequence lacks several amino caids at its N-terminal end and has additional amino acids at its C-terminal end when compared with the sequence shown in figure 9A-9C acids at its N-terminal end with the sequence shown in figure 9A-9C terminal end when compared with the sequence shown in figure 9A-9C compared with the sequence shown in figure 9A-9C compared with the sequence shown in figure 9A-9C compared with the sequence shown in figure 9A-9C compared with the sequence shown in figure 9A-9C compared with the sequence shown in figure 9A-9C compared with the sequence lacks at its C-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New STEAP (six transmembrane epithelial antigen of the prostate) proceins, expressed in human cancers, useful for detecting and t
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N-PSDB; AAD07072.
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                                                                                                                           New polynucleotide and polypeptides, useful for treatment and d of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, m sclerosis, diabetes and allergies.
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Best Local Similarity 83.2%;
Matches 272; Conservative
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(I) (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                             246 EEEYYRFYTPPNFVLALVLPSIVILDL 272
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                                                                                                                                                                                                                                                                                       QCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQ------ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1364.5; DB 5; Length 1082; Pred. No. 1.1e-137; 0; Mismatches 0; Indels 55;
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Run on:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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Gapop 10.0 , Gapext 0.5
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Match
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1: sp_archea:*
2: sp_bacteria:*
  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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5 8			5. 80			6.1	6.1	6.3	6. <sub>3</sub>	6.4	6.4	6.4	6.6	6.7	6.8	6.8	7.0	7.2	7.3	13.8	23.0	26.7	29.9	30.1	30.4	31.0	40.7	44.3
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## ALIGNMENTS

<sup>당</sup> 상	Db Qy	Query M Best Lo Matches	DR PI	DR GC	-		R1 80				RC TI			200					200	IUI
61 RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM 120 	1 MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS 60	Query Match 97.4%; Score 2290; DB 4; Length 490; Best Local Similarity 99.8%; Pred. No. 4.1e-176; Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps	Ptam; PF03807; F420 ox1dored; 1. SEQUENCE 490 AA; 56027 MW; D1971A84880F7E51 CRC64;	GO; GO: 0000118; F:election transport; ran. InterPro; IPR004455; NADPoxred_F420.	AAG32149.1;	ncer.";	s overexpressed in	ביין ביין ביין ביין ביין ביין ביין ביין	Korkmaz K.S., Elbi C.C., Korkmaz C.G., Loda M., Hager G.L.,	; PubMed=12095985;	TISSUE=Prostate;	D=9606;	Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	STAMP1.	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	(TrEMBLrel. 23, Last	01-MAR-2003 (TrEMBLrel. 23, Created)	QBIUE7 FREHIMINAKI; FKI; 350 AA.	
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01-OCT-2002 (TrEMBI
01-JUN-2003 (TrEMBI
01-JUN-2003 (TrEMBI
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"Cloning and characterization of a novel six-transmembrane protein
STEAP2, down-regulated in androgen-independent prostate cancer.";
submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF455138; AAN04080.1; -.
Genew; HCNC:17885; STEAP2.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420_oxidored; T.
Transmembrane.
SEQUENCE 490 AA; 55961 MW; F2E9C30CDACCEF81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                    RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
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LARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
                                                                             RINOYPESNAEYLASLEPDSLIVKGENVVSAWALQLGPKDASROVYICSNNIQARQQVIE
                                                                                                                 RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE
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Chordata; C
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
mbrane epithelial antigen of prostate 2.
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Pred. No. 1.2e-175;
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                                                                                                                                                                                                                                                                                                                                                         the RIXEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation," or ital-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AK052981; BAC55230.1; -.
EMBL, AK052981; BAC55230.1; -.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPOXTED, F4EM, PF03807; F420 oxidored; I.
Pfam, PF03807; F420 oxidored; I.
Pfam, PF03807; F420 oxidored; I.
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STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
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Pred. No. 4.8e-172;
9; Mismatches 2;
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Sciurognathi; Muridae;
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phathanalysis of the mouse transcriptome based on (60,770 full-length cDNAs.";
Nature 420:563-573(2002).
RMCD; MGC1:1915678; Tsap6.
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Q99P41; O1-JUN-2001 (TrEMBLrel 17,
01-JUN-2001 (TrEMBLrel 17,
01-JUN-2003 (TrEMBLrel 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel prostate cancer associated gene.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ
EMBL; AF335281; AAK00361.1; -
EMBL; AF238865; AAL78207.1; -
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54640 MW; 59FF07121919FDC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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STRAIN=Dunning, TISSUE-Prostatic carcinoma;
STRAIN=Dunning, T. Steiner M.S.;
Lu Y., Rinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
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                                                                                                        QIGLLSFFFAMLHALYSFCLPLRRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEIYLSL
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56.2%; Pred. No. 1.2e-97;
tive 81; Mismatches 100;
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Mus musculus (Mouse). Thordara: Craniata; Vertebrat
Q80ZF3;
Q80ZF3;
01-JUN-2003
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EMBL; BC037435; AAH37435.1; -.
MGD; MGI:1915678; Tsap6.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420 oxidored; I.
SEQUENCE 488 AA; 54749 MW; 9A08D99C9OCF83F4
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Mammalia; Eutheria;
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The p53 inducible TSAP6 gene product regulates apoptosis and cycle and interacts with Nix and the Mytl kinase.";

Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289 (2003).

EMBL; AY214462; AAO38239.1;

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SETTU V., Lamblin D., Lenoir C., Manivet
Kellermann O., Loric S.;

"Molecular cloning and expression of mot
Submitted (APR-2001) to the EMBL/GenBank
EMBL, AV029586; AAK50539.1; -.

MGD; MGI:1915678; Tsap6.

GO; GO:0006118; P:electron transport; IE
GO; GO:0006118; P:electron transport; IT
TherPro; IPR004455; NADPOXTED 4720.

Pfam; PF03807; F420 oxidored; I.
SEQUENCE 514 AA; 57268 MW; 339886C28
                                                                                                                                                                                                                                         Q86SP6 PRELIMINARY; PRT; 488 AA.
Q86SP6;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to dudulin 2 (TSAP6).
Homo sapiens (Human).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Kidney;
Strausberg R.;
Submitted (JAN-2003)
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SEQUENCE FROM N.A.
MEDILINE=25506415; PubMed=12606722;
Passer B.J. Nancy-Portebois V., A
Roborel de Climens A., Fiucci G.,
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Pred. No. 8.3e-97;
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    Prieur S.,
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"The p53-inducible TSAP6 gene product regulates apoptosis and Tcycle and interacts with Nix and the Mytl kinase.";

Proc. Natl. Acad. Sci. U.S.A. 100:2284-2289(2003).

R EMBL; BC042150; AAH42150.1; -.

R EMBL; BC0042150; AAH42150.1; -.

R EMBL; AY214461; AAO38238.1; -.

R EMBL; AY214461; AAO38238.1; -.

R EMBL; BC0006118; P:electron transport; IEA.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR004355; NADPoxred F420.

R InterPro; IPR004455; NADPoxred; I.

R PROSITE; P800290; IG_MHC; 1.

R PROSITE; P800290; IG_MHC; 1.
SEQUENCE FROM N.A.
TISSUB=Human colon endothel p
Bloecker H., Boecher M., Mewe
Pobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the E
EMBL; BX538047; CAD97986.1; -
Hypothetical protein.
SEQUENCE 498 AA; 55593 MW;
                                                                                                                                                                                                                                                                                              Q72389 PRELIMINARY; PRT; 498 AA. Q72389; O1-OCT-2003 (TrEMBLrel. 25, Created) O1-OCT-2003 (TrEMBLrel. 25, Last sequence up O1-OCT-2003 (TREMBLREL 25, Last annotation Hypothetical protein DKFZp686H07150.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Catarrhini; Hominidae;
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Best Local Sim
Matches 242;
"Dudulin 2, a new tumor antigen expressed in var Submitted (APR-2001) to the EMBL/GenBank/DDBJ da. RemBL, AKO01691; BAA91839 1; -- REMBL, AKO01691; BAA91839 1; -- REG, GO:0006118; P:electron transport; IEA. RINterPro; IPR003006; Ig MHC. RINterPro; IPR0030465; NADPoxred_F420. Refam; PF03807; F420 exidored; I. RPOSTT; PS00290; IG MHC; 1. RPOSTT; PS00290; IG MHC; 1. RPOSTT; PS00290; IG MHC; 1. SEQUENCE 488 AA; 54616 MW. BCORDANGE.
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Q9NVB5;
01-OCT-2000
01-OCT-2000
01-JUN-2003
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01-OCT-2000 (TrEMBLrel. 24, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ10829 (Dudulin 2).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Su
Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project ";
"NEDO human cDNA sequencing project ";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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larity 54.5%;
Conservative 8
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Pred. No. 4.4e-94;
                 BC0BCA483335AAD6
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Lu Y. Beheshti B., Squire J.A., Yang X.J.;

Lu Y., Beheshti B., Squire J.A., Yang X.J.;

"Characterization of a novel apoptosis inducing inhibits prostate cancer cell growth.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ de EMBL, AV082673; AMV5136.1;

GO; GO:0006118; Pielectron transport; IEA.
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Best Local S
Matches 239
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Steiner M.S., Allay J.A., Wang C.;

A Steiner M.S., Allay J.A., Wang C.;

Steiner M.S., Allay J.A., Wang C.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF238864; AAL78806.1; -.

R EMBL; AF238864; AAL78806.1; -.

R GO; GO:0066118; P:electron transport; IEA.

R InterPro; IFR003006; Ig_MHC.

R InterPro; IFR003455; NADPOxxed F420.

R InterPro; IFR004455; NADPOxxed F420.

R Pfam; FF03807; F420 Oxidored; I.

R PROSITE; PS00290; IG_MHC; 1.

R PROSITE; PS00290; IG_MHC; 1.
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Homo sapiens (Human),
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Q8TF03; O1-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
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                         MALAMGEMEVDMGSLASAWEVEAMPLRILLEAWKVPTLLALGIEVCEYAYNEVRDVLQPYV
                                                                      LARQUNFIPIDLGSLSSAREIENLFLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA
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01-JUN-2002
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"Second human member of phyde family, Human phyde II.";
submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF26232; AAM08128.1; -...
GO:0006118; P:electron transport; IEA.
InterPro; IPR003006; Ig MHC.
InterPro; IPR004455; NADPoxred F420.
Pfam; PF03807; F420_oxidored; I.
PROSITE; PS00290; IG MHC; I.
PROSITE; PS00290; IG MGC; I.
SEQUENCE 456 AA; 50430 MW; C5F7C7008D55251E CRC64;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Catarrhini; Hominidae;
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Q923B6, Q923B6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to hypothetical protein FLJ23153 (Tnfa-induced adipose-related protein).
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InterPro; IPR004455; NADPOxred F420.
Pfam; PF03807; P420 oxidored; I
PROSITE; PS00024; HEMOPEXIN; 1:
SEQUENCE 470 AA; 52994 MW; 6823E7682AC78B19 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EMBL; AK040760; BAC30696.1; -.
GO; GO:0006118; P:electron transport;
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STRAIN-EC79E/6J; TISSUE-Aorta, and Vein;
MEDIJINE-22354683; PubMed=12466851;
The FANTOM Consortium,
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Search completed: April 16, 2004, 12:40:39 Job time : 49 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Abu-Threideh J., Stoneking T., Langston Y., Maupin R.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Hubert R.S., Vivanco I., Chen E., Rastegar S., Leong K.,
Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B.,
Jakobovits A., Saffran D.C., Afar D.E.H.;
"STEAR: a prostate-specific cell-surface antigen highly expressed
human prostate tumors.";
Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UHE8; 095034;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
Six transmembrane epithelial antigen of pro
STEAP OR STEAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=20056277;
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TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text{9}\text
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WU14W BRAFL
GSHR PLAFT?
AAA1 MOUSE
VIL1 REOVD
HMC3 DESVH
WU14W BOVIN
YT25 CAEEL
GTR1 CHICK
NU4C CHICK
NU4C OCHO
VHL6 YEAST
YUK9 YEAST
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Minimum Maximum

BG

seq length: 0 seq length: 2000000000

Total number

o H

141681 seqs,

52070155 residues

Gapext 0

hits satisfying chosen parameters:

141681

Sequence: Title: Perfect score:

US-09-455-486-6 2351

procein

protein search, using sw

model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

9

Scoring table:

BLOSUM62 Gapop 10.0 ,

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

SwissProt\_42:\*

Result

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Length

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FSHR\_HUMAN FSHR\_PIG SOTB\_ECO51 SOTB\_ECO61 NPT1\_MOUSE NUCC\_NEPOL Y304\_BRUME Y301\_BRUME

STEA HUMAN F4RE METJA F4RE METTH FSHR MACFA Y538 PASMU FSHR CHICK FRE6 YEAST FRE7 YEAST

98 97.5 97.5 97.5 97

NUAM BRALA SPR1\_HUMAN POLG\_YEFV1 POLG\_YEFV2 YD49\_AQUAE FSHR\_BOVIN YG46\_XANAC FSHR\_RAT

FSHR RAT
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TRANSMEM 7:
TRANSMEM 11:
TRANSMEM 16:
TRANSMEM 21:
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Q58896;
01-NOV-1997
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EMBL; AC005053; AAC79150.1; ALT_INIT.
EMBL; AC004969; AAD15620.2; -.
EMBL; BC011802; AAH11802.1; -.
Genew; HGNC:11378; STEAP.
MIM; 604415; -.
MIM; 604415; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:000587; F:channel/pore class transporter ac
                                                         SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upo
10-CCT-2003 (Rel. 42, Last annotation upo
Putative F420-dependent NADP reductase
                        jannaschii.
Science 273
                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota;
Methanocaldococcaceae; l
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  haschii.";
ence 273:1058-1073(1996).
FUNCTION: Catalyzes the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLI
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Methanocaldococcus.
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Smith D.R., Doucette-Stamm I.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH; functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).
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Pfam, PF03807; F420 oxidored; I.
TIGRPAMS; TIGR00301; TIGR00301; 1.
Hypothetical protein; Oxidoreductase; NADP; Comp
SEQUENCE 223 AA; 24068 MW; 2370BBD6F5BBD3D9
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MEDLINE=98037514; PubMed=9371463;
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998 (Rel. 37, Last sequence update)
903 (Rel. 42, Last annotation update)
F420-dependent NADP reductase (EC 1.-.
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RESULT 4
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01-OCT-1993
28-FEB-2003
Follicle stir
MEDLINE-94071854; PubMed=7504463; Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.; Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.; "Molecular cloning of the testicular follicle stimulating receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis."; Biochem. Biophys. Res. Commun. 196:1066-1072(1993).

1- FUNCTION: Receptor for follicle stimulating hormone. 7 of this receptor is mediated by G proteins which activadenylate cyclase.
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                                                                                                                                                            SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Macaca.
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P32212;
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Pfam; PF03807; F420 oxidored; 1.
TIGRPAMs; TIGR00301; TIGR00301; 1.
Hypothetical protein; Oxidoreductase; NADP; Comp
SEQUENCE 232 AA; 24539 MW; Alce60ABC8474296
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stimulating hormone receptor precu
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llarity 23.8%;
Conservative 4
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                                                                                                                                                                                                                         eating macaque) (Cynomolgus monk
ata; Craniata; Vertebrata; Eutele
tes; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
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Pred. No. 0.02
12; Mismatches
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                                                                                                                                                                                                                                                                                                      precursor
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                  g hormone. The activity which activate
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InterPro; IPR00161; LRR.
InterPro; IPR00372; LRR_Nterm.
Pfam; PF00001; 7tm_1; 1.
Pfam; PF000560; LRR; 3.
Pfam; PF001462; LRRNT; 1.
PRINTS; PR00237; GPCRRHODOPSN.
SMART; SM00013; LRRNT; 1.
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                                                                                                                                                                                                                                                                                                                  DOMAIN
REPEAT
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein_coupled_receptor; Transmembrane;
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SIGNAL 1
                                                                                                                                                                                                                                                                                           REPEAT
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SIMILARITY: Belongs to
FSH/LSH/TSH subfamily.
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                     182
                                            157
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                                                                                         86
                                                                                                                 79
                                                                                                                                      84;
                                                                                                                                                   Similarity
                                                                                         HEIRIEKANNL-LYINPEAFQNLPNLRYLLISNTGIKHLPDVHKIHSFQKVLLDIQDNIN
                                                                                                                HEDALTKINII FVAIHREHYTSLWDLRHLLVG------KILIDVSNIMR
                     ARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYAR
                                                                  INQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIEL
---FNGTQLDELNLSDNNNLEELPNDVFHGASGPVILDISRTRIHSLPSYGLENLKKLRA
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199
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                                                                                                                                         Conservative
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                                            -TIERNŚFVGLSFESVILWL----NKNGIQEIHNCA
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                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR
7 (POTENTIAL).
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Pred. No. 0.9
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2 (POTENTIAL
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1 of G-protein cou
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MBL outstation -
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InterPro; IPR007916; UPF0191.
Pfam; PF05252; UPF0191; 1.
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=Pm70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical PM0538.
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                                                                                                                                                                                                                                                                                                                                           EMBL; AE006089; AAK02622.1; -.
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(Rel. 41, Last sequence up
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protein PM0538.
    Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                     EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=97057887; PubMed=8902217;
You S., Bridgham J.T., Foster D.N., Johnson A.L.;
"Characterization of the chicken follicle-stimulating k
receptor (cFSH-R) complementary deoxyribonucleic acid,
cf cFSH-R messenger ribonucleic acid in the ovary.";
Biol. Reprod. 55:1055-1052(1996).
Biol. Reprod. 55:055-1052(1996).
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                                                                                                                                                                                                                             the Buropean Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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FSH/LSHTY: Contains 7 leucine-rich (LRR) repeats.
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P23945;
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InterPro; IPR000276; GPCR\_Rhodpsn. InterPro; IPR001611; LRR. InterPro; IPR000372; LRR\_Nterm. Pfam; PF00001; 7tm\_1; 1.

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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
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                                KQDLGEQTGKRKHRRSAAEDYISHYGTRFGPVENEFDYGLCNEVVDFVCSPKPDAFNPCE
                                                                                                FIKKLRARSTYKLKKLP--DVNKFRSLIEANFTYPSHCCAFTNRKTQNTEFYPICSMSPA 297
                                                                                                                                 VIHPYARNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGL-------
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17.2%;
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K-> R (I
N -> S (I
N -> S (I
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G -> A (IN REF. 2).
X -> R (IN REF. 2).
Y -> L (IN REF. 2).
V -> L (IN REF. 2).
V -> L (IN REF. 2).
V -> L (IN REF. 2).
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red. No. 0.87;
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 ---YSLCLPMRRSERYLFLNMAYQQVHAN 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 693;
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Q12473;
15-DEC-1998
15-DEC-1998
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97313267; PubMed=9169871;
Johnston M., Hillier I., Riles L., Albermann K., Andre B., Ansorge V., Struckner M., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Louis E.J., Messenguy F., Mews H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M. Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose J. Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Vierendeels F., Voet M., Volckaert G., Voss H., Wambbutt R., Wedler H., Zimmermann F.X., Zollner A., Hani J., Hohelsel J.D.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII
                                                                  EMBL; Z47973; CAA88006.1; -.
EMBL; Z73156; CAA97503.1; -.
PIR; S50969; S50969.

GermOnline; 142046; -.
SGD; S0003974; FRE6.
InterPro; IPR002916; Ferric_reduct.
Pfam; PF01794; FRE7ic_reduct; 1.
Oxidoreductase; Electron transport; Transmembrane; FAD; NAD; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a continuous of the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                               Nature 387:87-90(1997).

-i- CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+)

-i- COFACTOR: FAD (Probable).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    i5-DEC-1998 (Rel. 37, Created)
i5-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ferric reductase transmembrane component 6 precursor
NP_BIND
                                    FAD; NJ
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein -!- SIMILARITY: Belongs to the FRE / CYBB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota;
Saccharomycetales; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Ferric-chelate reductase 6). FRE6 OR YLL051C OR L0593.
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Matches 72
SEQUENCE FROM N.A.
STRAIN=5288C / FY1679;
MEDLINE=96132030; PubMed=8553699;
MEDLINE=96132030; PubMed=85.53699;
Casamayor A., Aldea M., Casas C., Her
Laftuente M.J., Gancedo C., Arino J.;
"DNA sequence analysis of a 13 kbp fx
Chromosome XV containing seven new op
Yeast 11:1281-1288(1995).
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                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                    NCBI_TaxID=4932;
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72; Conserv
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Pred. No. 0.9;
1; Mismatches 119
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                    fragment of the left open reading frames."
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                          frames."
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RESULT 9
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CARBOHYD
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Germonline; 143574; -.

SGD; S0005512; FRE7: reduct.

InterPro; IPR002916; Ferric reduct.

Pfam; PF01794; Ferric reduct; 1.

Oxidoreductase; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                   FSHR HUMAN STANDARD; PKT; 575 AM
P23945; Q16225;
01-MAR-1992 (Rel. 21, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last amotation update)
Follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAD; NAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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EMBL; Z74894; CAA99174.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                    FSHR.
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Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                            receptor).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + COFACTOR: FAD (Probable).
SUBCELLULAR LOCATION: Integral membrane protein
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                                                                                                                                                                                                                                                                                                                  176
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                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                   GPVVVAISLATEFFLYSFYRDVIHPYARNQQSDFYKIPIBIVNKTLPIVAITLLSLYY-L
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                                                                                                                                                                          AVKGYLRÞGRSFMÅSTIANVSÍV 334
                                                                                                                                                                                                                                            --SVSNALNWREFSFIQSTLGYVALLISTFHV--
                                                                                                                                                                                                                                                                     LROARH---EGGYERMH----QRWKASDMWR----
                                                                                                                                                                                                                                                                                                                   SGKINVIGWLVGLSYE----KINIYHQW-----
                                                                                                                                                                                                  ----FYTPPNFVLALVLPSIVIL 444
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71996
  Chordata;
Primates;
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21.7%;
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N-LINKED (GLCNAC. . .) (P
; 2384480E9289C16F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 107.5;
Pred. No. 1;
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  Craniata; V
Catarrhini;
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                                                         update)
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   Vertebrata;
i; Hominidae;
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                                                           (FSH-R)
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              Euteleostomi;
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                                                             (Follitropin
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6 outstation -
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3D-STRUCTURE MODELING OF 49-228.
MEDLINE=06363672; PubMed=8747461;
Jiang X., Dreano M., Buckler D.R., C.
Hendrickson W.A., el Tayar N.;
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hormone receptors and the nature of
Structure 3:1341-1353(1995).
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Shaw N., L
Friedland
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MEDLINE=99318093; PubMed=10391209;

Cargill M., Altshuler D., Ireland J., Sklar P.,

Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., 1

Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., 1

Friedland L., Rolfe A., Warrington J., Lipshutz
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TISSUE=Te
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Tilly L.T., Aihara T., N
Kowalski K.I., Perlas E.
Submitted (XXX-1992) to
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"Characterization of the 5' flanking re; 
stimulating hormone receptor gene."; 
Mol. Cell. Endocrinol. 102:93-102(1994)
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MEDLINE=95011044;
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Cell. Endocrinol. 89:141-151
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Cheng S.V., Nugent N.P.,
L., Overton S.A., Wands G.
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EMBL; S73199; AAB32071.1
EMBL; S73526; AAB32223.1
EMBL; S73561; ORHUFT.
DB; 1XUN; 15-MAY-97.
Genew; HGNC:3969; FGHR.
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VARIANT OHSS ASN-567.
WEDLINE=22812037; PubMed=12930928;
MEDLINE=2794Funbosun O., Delbaere
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Smits G., Olatumb
Costagliola S.;
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FUNCTION: Receptor for follicle stimulating of this receptor is mediated by G proteins v adenylate cyclase.

SUBCELLULAR LOCATION: Integral membrane prot.

ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=1
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MIM; 608115; -.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0005886; C:plasma membrane; TAS.

GO; GO:0004963; F:follicle stimulating hormone recept

GO; GO:0007292; F:female gonad development; TAS.

GO; GO:0007186; F:female gonad development; TAS.

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Pfam; PF01462; LRRNT; 1.

PRINTS; PR00237; GPCRRHODDESN.

SMART; SM00013; LRRNT; 1

PROSITE; PS00237; G PROTEIN RECEP_F1_2; 1.

PROSITE; PS00262; G PROTEIN RECEP_F1_2; 1.

PROSITE; PS00262; GPROTEIN RECEP_F1_2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; S

G-protein coupled receptor; Transmembrane; Alternative
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0276; GPCR_Rhodpsn.
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PRINTS; PR00237; GPCRHODOPSN.
SMART; SM00013; LRRNT; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
GG-PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
GG-PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
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Remy J.J., Lahbib-Mansais Y., Yerle M.,
Pajot E., Grebert D., Salesse R.;
"The porcine follitropin receptor: cDNA
expression and chromosomal localization
                                                                                                                                                                                                           EMBL; L31966; AAA86933.1;
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la Barbera A.R.;
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Mammalia; Eutheria;
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This SWISS-PROT entry is copyright. It is produced through a obstween the Swiss Institute of Bioinformatics and the EMBL
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15-MAR-2004
This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar
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SIMILARITY:
(TC 2.A.1.2)
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Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Lin J., Yen G., Schwartz D.C., "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugar efflux transporter.
SOTB OR Z2173 OR ECS2135.
Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                           MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Iida T., Takami H., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. B:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhaw G.F., Evans P.S., Gregor G., Kirkpatrick H.A. Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L. Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodeca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                  DNA Res. 8:11.22(2001).

- FUNCTION: Involved in the efflux of sugars. The physiological rolar refunction of the intracellular concentration of toxic may be the reduction of the intracellular concentration of toxic sugars or sugar metabolites. Transports L-arabinose and to a lesser extent IPTG. Seems to contribute to the control of the arabinose regulon (By similarity).

- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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STRAIN=0157:H7 / E
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(Rel. 41, Last sequence update)
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RESULT 12
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ID SOTB ECOLI STANDARD; PRT; 396
AC P31122; P76883; P77333;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence upda
DT 15-MAR-2004 (Rel. 43, Last annotation up
DE Sugar efflux transporter.
GN SOTB OR B1528.
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Best Local &
Matches 85
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rPro; IPR005828; Sub_t; PF00083; sugar_tr; ]
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t; Sugar transport;
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BAB35558.1;
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      STRAIN=K12;

STRAIN=K12;

MEDLINB=97251357; PubMed=9097039;

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Ito
Alba H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,

Kasai H., Kashimoto K., Mirobuchi K., Mori H., Mori T., Motomura K.,

Makino K., Miki T., Mirobuchi K., Mori H., Mori T., Motomura K.,

Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sail

Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

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corresponding to the 28.0-40.1 min region on the linkage map.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97426617; PubMed=9278503;
Blatther F.R., Plunkett G. III, Bloch C.?
Riley M., Collado-Vides J., Glasner J.D.,
Gregor J., Davis N.W., Kirkpatrick H.A.,
Mau B., Shao Y.;
The B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                     Carole S., Pichoff S., Bouche J.-P.,
"Bscherichia coli gene ydeA encodes a major facilitator pump which
exports L-arabinose and isopropyl-beta-D-thiogalactopyranoside.";
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J. Bacteriol. 181:5123-5125(1999).
J. Bacteriol. Involved in the efflux of sugars. The physiological repurction of the intracellular concentration of to a sugar or sugar metabolites. Transports L-arabinose and to a lesser extent IPTG. Seems to contribute to the control of the
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STRAIN=K12 / MG1655;
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        EMBL;
EMBL;
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                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=99194728; PubMed=10094697;
Bost S., Silva F., Belin D.;
"Transcriptional activation of ydeA, which encodes a memb
major facilitator superfamily, interferes with arabinose
and induction of the Escherichia coli arabinose PBAD prom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99369894; PubMed=10438792; Carole S., Pichoff S., Bouche J.-P
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-JS219;
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MEDLINE=93186717; PubMed=8383113;
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SUBCELLULAR LOCATION: Integral membrane (Probable).
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nce 277:1453-1474(1997).
        D90795;
D90796;
D90797;
                                                     AE000250; AAC74601.1;
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J.D., Rode C.K., M
.A., Goeden M.A.,
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protein. superfamily.

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PIR; C64907; C64907.
Ecogene; EG11636; sotB.
HAMAD; MF 00507; 1.
                               01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Renal sodium-dependent phosphate transport protein 1 (Sodium/phosphate cotransporter 1) (Renal sodium-phosphate transporter 1) (Renal Na(+)/pl cotransporter 1) (Renal Na(+) dependent phosphate cotransporter transport protein 1) (Renal Na(+) dependent phosphate cotransporter
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Transport; Sugar transport;
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18.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 396;
                                                                                                                                                                                                                                                                                                                                          ----ALNWREFSFIQST
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                                                                     (Sodium/phosphate
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Bourdeau J.E., Hughes M.R.;
"Cloning, genetic mapping
sodium-depender"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, genetic mapping, and expression analysis of a mous sodium-dependent phosphate cotransporter.";

Am. J. Physiol. 268:F1038-F1045(1995)

I- PUNCTION: Important for the resorption of phosphate by to the many be involved in actively transporting phosphate into Na(+) cotransport in the renal brush border membrane.

SUBCELLULAR LOCATION: Integral membrane protein.

ITSSUE SPECIFICITY: Kidney.
                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM TRANSMEM CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X77241; CAA54459.1;
PIR; S69915; S69915.
MGD; MGI:103209; Slc17a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007114; MFS.
InterPro; IPR004745; Pi_cotranspt.
TIGRFAMs; TIGR00894; 2A0114euk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                   269
                                                  246
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                                                                                                                                                                                                                                                                                                                                  Similarity
--LVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPMR
                                                                                                                                                                                                              ICSNNIQARQQVIELARQLNFI----PIDLGSLSSAREIENLFLRLFTLWRGPVVV----
                                                                                                                                                                                                                                                                             GKILIDVSNNWRINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDA---SRQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50850; MFS;
                                                  SGRQSLPİKAMLKSLPLWAİILNSFAFIWSNSLLVTYTPTFISTVLHVNVRENGLLSSLP
                                                                                                                 GFICDLLGWPMVFYIFGIVGCVLSLSWFFLFFDDPKD--HPYMSSSEKDYIISSLMQQAS
                                                                                                                                                                                  VCRVLQGIAQGTVSTGQHEIWVKWAPPLERGRLTS-----MTLSGFVM--GPFIVLLVS
                                                                                                                                                                                                                                                 GLILSSVFFGMVVVQAP----VGYLSGIYPMKRIIGSSLFLSSLMSLLIPPAAQVGAALVI
                                                                                ---YKIPIEIVNKTLPIVAITLLS
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39 N
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51589 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium
                                                                                                                                                                                                                                                                                                                  4.4%; Score 103; DB 1;
18.7%; Pred. No. 1.5;
tive 64; Mismatches 14;
                                                                                                                                                   ------AISLATFFFLYSFVRDVIHPYARNQQSDF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions on ng as its content is in no ved. Usage by and for commer
                                                                                                                                                                                                                                                                                                                    142;
                                                                                                                                                                                                                                                                                                                                                Length 465;
                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and the EMBL outstation
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MEDLINE=99398694; PubMed=10468594;
Turmel M., Otis C., Lemieux C.;
"The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con entitles requires a license agreement (See http://www.isb-sib.ch/aror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorodendrales; Chlorodendrales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
NAD(P)H-quinone oxidoreductase chain H, Chloroplast (EC 1.6.5.-)
NAD(P)H-quinone oxidoreductase chain H) (NADH-plastoquinone oxidoreductase
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001135; Oxidored_49kDa.
Pfam; PF00346; Complex1 49kd; 1.
PROSITE; PS00535; COMPLEX1_49k; 1.
Oxidoreductase; NAD; NADP; Quinone; Plastoquinone; Chloroplast SEQUENCE 391 AA; 44913 MW; 9A40AEC68995B25E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF137379; AAD54891.1;
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kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) + plastoquinol. SIMILARITY: Belongs to the complex I 49 kDa subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIR CHAIN. THE IMMEDIATE BLECTRON ACCEPTOR FOR THE ENZYME:
TO BE PLASTOQUINONE. COMPONENT OF THE IRON-SULFUR (IP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO BE PLAST
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                                                                                           --SNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQL
                                                                                                                                                                                              KTNIIFVAIHREHYTSLWDLRHLLV---GKILID-----
NFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYARNQQS
                                                 KTDPMIVSM-GPHHPSMHGVLRLIVTLDGENVLDCEPVVGYLHRGMEKIAENRTIVQYLP
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Chlorodendraceae; Nephroselmis
                                                                                                                                                                                                                                                                     4.4%;
                                                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                     Score 102.5;
Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96:10248-10253(1999).
TTRONS FROM NADH TO THE RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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       245
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     RESULT 15
Y304 BRUME
ID Y304 BRU
AC Q8YD73;
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DT 28-FEB-:
DT 28-FEB-:
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DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza N. Bernal A. Mazur M., Goltsman Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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-!- SUBCELLULAR LOCATION: Integral membrane pr
-!- SIMILARITY: Belongs to the UPF0191 family.
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Pfam; PF05252; UPF0191; 1.
Pfam; Pr05252; UPF0191; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement
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Search co Job time	ממ	γQ	Дb	Ş	Db	γŞ	Db	γŞ	Query N Best Lo Matches
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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb A;Reference number: Z20556; MUID:97000351; PMID:8843436

A;Accession: T50571
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C;Species: Streptomyces coelicolor
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C;Accession: T50571
R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kina
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A; Residues: 1-211 < KUR>
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2560
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C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. strain PCC 7120 is a synonym of An C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #t C;Accession: AC2560 R;Kaneko, T.; Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, Y.; Wolk, C.P.; Kuritz, T.; S. Nakkamura, 
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A;Experimental source: strain A3(2)
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A;Experimental source: strain PCC 7120
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; Yasuda, M.; 'Milakasaki, N.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasuda, M.; Yasud
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ETARRSDVVIVAVPWDGHGKTLESLRAELSGKLVVDCVNPLGFDKKGAYALKPEEGSAAE
                                                                                                                                                                                                          LPDVSGLVVGVLGGTGPQGKGLAYRLAKAGQKVIVGSRAAERAAAAEEIGHGVEGADNA
                                                                                                                                                                                                                                                                                                            IKDARKVTVGVI-GSGDFAKSLTIRLIRCGYHVVIGSR---NPKFASEFFPHVVDVTHHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein MJ1501
                                                                                                                                                                                                                                                                                                                                                                                                         6.7%; Score 156.5; DB 2; llarity 27.9%; Pred. No. 5e-05; Conservative 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.9%;
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; Pred. No. 2.4e-05;
43; Mismatches 70;
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#text_change 09-Dec-2002
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Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch: A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69400
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A; Residues: 1-213 < KLE>
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Best Local S
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                                                 191
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179
                                                                                                     120
                                                                                                                                                132 YLASLFPDSLIVKGENVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFI-PI 190
                                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                       67 --VAV----FTIPWEFAFDTAEMLKRQLAGKVVISPLVPMKKVGDNF-VYVRPEEGSAAE 119
                                                                                                                                                                                                                                                     89 IFVAIHREHYTSLWD------LRHLLVGKILID-----VSNNWRINQYPE--SNAE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Zhou, L.; Overbeek, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                              56; Conserv
                                                 DLGSLSSAREIENL-PLRIFTLWR 213
                                                                                                                                                                                                                                                                                                            GTGNLGEGLALRWGKLGYEIIVGSRKLEKAEKLASDYLKKVGDASIIGMRNEDAAETCD- 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAAALLPDSRVAAAFHHLSAVLLQDPEIDEIDTDVMVLGEERADVEI---
                                                                                                                                                                                                                                                                                                                                                           GSGDFAKSLTIRLIRCGYHVVIGSRN----PKFASEFFPHVVDVT----HHEDALTKTNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLASLFPDSLIVKGFNVVSAWALQ-----
DAGGLSNAHLVESLTPLILNVMKR 202
                                                                                                  KLASVLEESSVVAAYHSIPARRFANLGEEFEWDVPICGDS-GAKEVVVDLTEKISGLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LAGR----IPGMRGVFAGRLRNAHQVESLVANLISVNR 226
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            6.3%; Score 147; DB 2;
27.5%; Pred. No. 0.00024;
tive 44; Mismatches 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 213
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RESULT D69361

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69361 archaec

translation not

A;Status: preliminary; nucleic acid sequence not shown; tran A;Molecule type: DNA A;Residues: 1-212 <KLE> A;Cross-references: GB:AE001042; GB:AE000782; NID:g2689365; C;Superfamily: conserved hypothetical protein MJI501 PIDN:AAB90348.1; PID:g264970

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C;Species: Methanobacterium thermoautotrophicum
C;Bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_ci
C;Bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_ci
C;Accession: T10120
R;Berk, H.; Thauer, R.K.
PEBS Lett. 438, 124-126, 1998
A;Title: F420H2:NADP oxidoreductase from Methanobacterium
A;Reference number: Z16959; MUID:99037734; PMID:9821972
A;Accession: T10120
A;Accession: T10120
A;Accession: T10120
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blaireich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannas
                                                                                                                    RESULT 7

16.4487
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: D64487
C;Accession: D64487
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A;Experimental source: strain Marburg
C;Superfamily: conserved hypothetical
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F420-dependent NADP reductase (EC 1.6.8.-) - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
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A; Residues: 1-224 <BER>
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Best Local S
Matches 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTK--TN------
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                                                                                                                                                                                                                                                                                                                     IDLGSLSSAREIENLPLRLFTL
                                                                                                                                                                                                                                                                                                                                                                                                              SLFPD--SLIVKGFNVVSAWALQ--LGPKDASRQVYICSNNIQARQQVIELARQLNFI-P 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVAILTVPLQAQMAT-LGSVKEAIKGKVLIDATVPIDSCLGGSAVRYIDLWDGSAAERAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IIFVAIHREHYTSLWDLRHLLVGKILIDV-----SNNMRINQYPESNAEYLA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGDQGLGLALRLALAGEEVIIGSRDAEKAVSAAQKVLEIAERDDLKVKGATNAEAAEEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 142; DB 2; Length 22 llarity 29.2%; Pred. No. 0.00064; Conservative 29; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                         206
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dek, A.
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A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-223 <BUL> A;Cross-references: GB:U67591; GB:L77117; NID:g2826422; PIDN:AAB9951 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The complete genome sequence of the lactic acid k;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: P86826 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein yqfE [imported] - Lactococcus lactis subsp. lactis (st C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: F86826
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F86826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A64300; MUID:96337999; PMID:8688087 A;Accession: D64487
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE005176; PID:g12724621; PIDN:AAK05712.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yqfE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1~191 <STO>
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Best Local S
Matches 46
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Best Local S
Matches 47
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                                                                                                                                                                     43 VVLAVPYVAIAGIIQEYSTD-----LQGKIIIDITNPVDFTTFDSLLVPSDTSAAALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 5.7%; Score 133; DB 2
l Similarity 21.9%; Pred. No. 0.0033
46; Conservative 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                              ASLFPDSLIVKGFNVVSAWALQLGFKDASRQ----VYICSNNIQARQQVIELARQLNFIF 189
                                                                                                                                                                                                                                                           TISIFGKGKMGKAI-----
                                                                                                                                                                                                                                                                                                  TVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVDVTHHEDALTKTN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGDVVILSLPYEYTLSTIKQLKEELKGKIVVSIGVPLATAIGDKPTRLLFPPDGSVÄEMV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFFHVVDV------THHEDALT
LDAGSLKRARELEAIGFLQITLAASEKISWDG 185
                                                                              -----IIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPE-----
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                                       IDLGSLSSAREIENLPLRLFTL--
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                                       -- WRG 214
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A;Gene: MTH248
A;Start codon:
C;Superfamily:
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T00121
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MJID:98037514; PMID:9371463

A;Accession: A69131
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R;Takahashi, Y.; Akase, K.; Hirano,
Gene 215, 37-45, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 8 - Leptospira int
C;Species: Leptospira interrogans
C;Date: 22-Jan-1999 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, i, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                            Molecule type: DNA
                                                                                                                                                                                                                                                   Residues: 1-216 <TAK>;Cross-references: EMBL;AB010203; NID:g2780763; PIDN:BAA24368.1; PID:g2780765;Experimental source: strain Ictero No.1; substrain icterohaemorrhagiae
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49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein 8 - Leptospira interrogans
                                                                                                                                                                                                  Similarity
                                   VLCSKGSVASEVLTLSGIDSLNGKTIIDTTNPISEIPPQNGVLNFFTSYNESLMEKLQKQ 125
                                                                                                                                              VGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASBFFPHV---VDVTHHEDALTKTNII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDAAASADVVVLTVPLQAQMVTLASIRDQVRDKVLIDATVPIDSCIGGSAVRYIDLWEGS
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FPDSLIVKGFNVVSAWALQLGP--KDASRQVYICSNNIQARQQVIELARQLNFIPIDLGS 194
                                                                        FVAIHREHYTSLWDLRHL--LVGKILIDVSNNMR----
                                                                                                           IGILGSGIVGQTLANGFLKYGAEVKIGTRDFGKLKDWLAKAGAGASIGSFSEAANFGEII
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                     genetic maps of the Leptospira interrogans
                                                                                                                                                                                                  5.1%; Score 119.5; DB 2; 23.7%; Pred. No. 0.037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein MJ1501
                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-Jan-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                    PMID:9666070
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 C;Date: 11-Jan-2002 #sequence_revision C;Accession: AB3182 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; erage, G.; Gillet, W.; Grant, C.; Guent; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                              RESULT
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                                                                                                           conserved hypothetical protein Atu5183 [imported] - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
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A,Experimental source: strain 945c

R,Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, E

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr

Chado, M.A.; Madeira, A.M.S., Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.,

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; de Sa, M.S.; Silva Jr., W.A.; da Silva, M.,

A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein XF1737 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G88642
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleot Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A88515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                                                                LFPDSLIVKGFNVVSAWALQLGPKDASRQ-----VYICSNNIQARQQVIELARQLNFIFI 190
IVGNLAAAASFQ
                                                             DLGSLSSAREIE
                                                                                                                             YMPGARLVRAFSAVDATVVE---TSASRRGGRIGMPLASDDAEAMKVAEGLVRDAGCDPV
                                                                                                                                                                                                                                                    EFGTVLLLAVPFEALPQVGRDLRGAYRGKIVLDSTNPWGASSADVYREARELGVAQTVVK 148
                                                                                                                                                                                                                                                                                                                  TKTNIIFVAIHREHYTSLW-DLRHLLVGKILIDVSNNMRINQ---YPESN----AEYLAS
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24.0%; Pred. No. 0.0;
tive 40; Mismatches
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; Guenthner,

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Kutyavin, Chen, L.;

Wood, G.E.; Chen, I.; Levy, R.; Li,

Monks,

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11-Jan-2002 #text\_change 18-Nov-2002

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A;Description: receptor that mediates the biochemical effects of follitropin A;Description: receptor; plycoprotein, leucine-rich alpha-2-glycoprotein; c;Keywords: G protein coupled receptor; glycoprotein; hormone receptor; phosphoprotein; F;1-17Domain: signal sequence #status predicted csIG>
F;18-695/Product: follitropin receptor #status predicted <PFH>
F;18-695/Product: follitropin receptor #status predicted <PFH>
F;18-695/Product: follitropin receptor #status predicted <PFH>
F;19-109/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F;96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F;121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F;194-218/Domain: transmembrane #status predicted <TM1>
F;399-421/Domain: transmembrane #status predicted <TM2>
F;444-465/Domain: transmembrane #status predicted <TM3>
F;446-50/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM5>
F;574-597/Domain: transmembrane #status predicted <TM5>
F;609-630/Domain:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: JN0898; S36452
R;Gromoll, J.; Dankbar, Sharma, R.S.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 196, 1066-1072, 1993
A;Title: Molecular cloning of the testicular follicle stimulating hormone receptor
A;Reference number: JN0898; MUID:94071854; PMID:7504463
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A;Cross-references: GB:AE008687; PIDN:AAL45872.1; PID:g17743615; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
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A;Genome: plasmid
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A; Accession: AB3182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-695 < GRO>
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22.7%; Pred. No. 0.063;
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R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, submitted to the EMBL Data Library, August 1995
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm A;Reference number: S59677
                                                                                                                                                                                                                                                                                          RESULT
S59681
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                                                                A;Molecule type: DNA
A;Residues: 1-1228 <HAL>
A;Cross-references: EMBL:U33335; NID:g965076; PID:g965081;
                                                                                                                                                                                                                                                         probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein LPA5w; hypothetical protein YP8132.01
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A; Reference number: A; Accession: S52519
              R;Badcock, K.; Churcher, C
submitted to the EMBL Data
A;Reference number: S52519
                                                                                                                     A; Accession: S59681
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Best Local S
Matches 84
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17.0%; Pred. No. 0.71
tive 75; Mismatches
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                                                                     MIPS:YPL012w
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A;Molecule type: DNA A;Molecule type: DNA A;Residues: 220-1228 <BAD> A;Cross-references: EMBL:Z48483; NID:g683777; PID:g683778; MIPS:YPL012w A;Cross-references: EMBL:Z48483; NID:g683777; PID:g683778; MIPS:YPL012w

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C;Keywords: transmembrane protein F;125-141/Domain: transmembrane #status predicted F;478-494/Domain: transmembrane #status predicted F;478-494/Domain: transmembrane #status predicted

A;Gene: SGD:RRP12 A;Cross-references: A;Map position: 16L

SGD:S0005933

	4.7%; Score 110.5; DB 2; Length 222; ilarity 24.3%; Pred. No. 0.2; Conservative 34; Mismatches 94; Indels 25; Gaps 6	Query Match Best Local Similarity Matches 49; Conser	3 B O
Inilarity 19.9%; Pred. No. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 15; Dec. 1	A. 97, 12176-12181, 2000 A. 97, 12176-12181, 2000 Y., C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Halbacterium species NRC-1. MUID:20504483; PMID:11016950 MUID:20504483; PMID:11016950  90thetical protein MJ1501	ad., S., S., S., S., S., S., S., S., S., S	Procus A; Au A; Re: A; Re: A; Re: A; Re: A; Re: C; Ge: A; Ge: C; Ge:
ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2:  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2:  11 KSLSETLEPNOINGIXDARK	7c [imported] - Halobacterium sp. NRC-1 , NRC-1 , NRC-1 (ce_revision 02-Feb-2001 #text_change 16-Feb-2001 Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.	rote obac -200 8441 nned	RESUL B8441 hypot C;Spe C;Dat C;Acc R;NG; ; Lei
t Local Similarity 19.9%; Pred. No. 1.5; Indels 225; Gaps 226; Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 21; KSLSSTCLPNGINGIXDARK	YRIIT 76	55 ALIQ	Дb
Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Conservative 71; Mismatches 152; Indels 225; Gaps 2: Conservative 71; Mismatches 152; Indels 225; Gaps 2: Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2: Ches 111; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 71; Conservative 72; Conservative 72; Conservative 72; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conservative 74; Conserva		10 VI	γQ
t Local Similarity 19.9%, Pools No. 1.5, between the Local Similarity 19.9%, Pools No. 1.5, between the Conservative 71; Mismatches 152; Indels 225; Gaps 11 KSLSETCLPNGINGIKDARK	LLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFH 40	52 EE 05 ES	å S
t Local Similarity 19.9%, Pocce No. 1.5;  t Local Similarity 19.9%, Pocce No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps  11 KSLSETCLPNGINGIKDARK	YTQTTPNARSYILETIDQYLKITSKEDLEKTFNNVCGLLKNSMNE 7	: 49 STNLLA	망
t Local Similarity 19.9%, Proc. No. 1.5;  t Local Similarity 19.9%, Proc. No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps  11 KSLSETCLPNGINGIKDARK	CHALKVLAESNVSYAEESSSHNVLLLQRFPISEAQKNIEYLSTK 6 VHVAYSLCLFMRRSERYLFLNMAYQQVHANIENSWNE 3	94 LÝSEVE 04 OLGILS	8 B
t Jocal Similarity 19.9%, Proc. No. 1.5, believe 115, ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 11 KSLSETCLPNGINGIKDARK	AGLLAAAYQLYYGTKYRRFPPWLETWLQCRK 3	70 VYL-	Ş
t Local Similarity 19.9%; pred. No. 1.5;  t Local Similarity 19.9%; pred. No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLSETCLENGINGIKDARK	PIETVNKTLP	37 HP	g 89
t Local Similarity 19.8%, Pred. No. 1.5,  t Local Similarity 19.9%, Pred. No. 1.5,  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLSETCLPNGINGIKDARK	ARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVI 23                 : : :           : : : :	89 P	B 8
t Local Similarity 19.9%, Pred. No. 1.5,  t Local Similarity 19.9%, Pred. No. 1.5,  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLSETCLPNGINGIKDARK	:  ::  :: : eeQfMDLRNEIELVIGASISAMG 48	57	g
t Local Similarity 19.9%; pred. No. 1.5;  t Local Similarity 19.9%; pred. No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLGETCLPNGINGIKDARK	VVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFI 18	38 PDSL	Š į
t Local Similarity 19.9%; pred. No. 1.5;  t Local Similarity 19.9%; pred. No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLGETCLPNGINGIKDARK	IIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLF 13	84 09 EIISQI	용 성
t Local Similarity 19.9%; pred. No. 1.5;  t Local Similarity 19.9%; pred. No. 1.5;  ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2  11 KSLSETCLENGINGIKDARK	HVVIGSRNPKFASEFFPHVVDVTHHEDAL	51 R 52 RKIP	유
t Local Similarity 19.9%; Pred. No. 1.5; ches 111; Conservative 71; Mismatches 152; Indels 225; Gaps 2		11 KSLSETCL  :::   : 92 KTMAETTI	g 8
2 Martin	4.7%; Score 111.5; DB 2; Length 1228; 19.9%; Pred. No. 1.5; ive 71; Mismatches 152; Indels 225; Gaps 2	ry Match t Local Similarit ches 111; Conse	Qu Ma

Search completed: April 16, 2004, 12:41:12 Job time : 23 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

RESULT 1

US-09-888-257A-10

Sequence 10, Application US/0988257A

Publication No. US2030060612A1

APPLICANT: Goddwski, Paul J.

APPLICANT: Goddwski, Paul J.

APPLICANT: Goddwski, Paul J.

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APPLICANT: Wodk, Victoria

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APPLICANT: Wodk, Victoria

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APPLICANT: Wodk, William I.

APPLICANT: Wodk, William I.

APPLICANT: Wolkis, Paul

APPLICANT: Wodk, William I.

APPLICANT: Wodk, William I.

APPLICANT: Wodk, William I.

APPLICANT: Wodk, William I.

APPLICANT: Wolfords

William I.

APPLICANT: Wolfords

William I.

APPLICANT: Wolfords

William I.

APPLICANT: Wolfords

INTILE OF INVENTION: CREATMENT OF TUMOR

FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: US/09/888, 257A

CURRENT FILING DATE: 1998-09-10

PRIOR APPLICATION NUMBER: US/09/888, 257A

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PRIOR APPLICATION NUMBER: PCT/US99/20111

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PRIOR APPLICATION NUMBER: PCT/US00/04342

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PRIOR APPLICATION NUMBER: PCT/US00/04343

PRIOR APPLICATION NUMBER: PCT/US00/04343

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PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/23328
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PRIOR PILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 10
PENGTH: 454
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                                                                                                                                                                                                                                                                        Sequence 3, Application US/10455822 Publication No. US20040048798A1 GENERAL INFORMATION:
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Best Local
                                                                                                                                                                           APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia
APPLICANT: Faris, Mary

TITLE OF INVENTION: Nucleic acids and Corresponding Prote

TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment

FILE REFERENCE: 51158-20016.24

FILE REPERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigne

PRIOR FILING DATE: 2002-12-20

PRIOR PRIOR FILING DATE: 2002-04-05
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; SEQ ID NO 3
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo s
US-10-455-822-3
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and Det
FILE REFERENCE: 51158-20016.34
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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Sequence 7, Application US/10455822
Publication No. US20040048798A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%;
Matches 454; Conservative C
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Pred. No. 6.1e-222;
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WESULT 4
US-10-455-822-9
(Sequence 9, Application US/10455822)
(Sequence 9, Application No. US20040048798A1
(Publication No. US20040048798A1
(GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Shtitled 98P4B6 Useful in Treatment and Dete
(TILE REFERENCE: 51158-20016.24
(CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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TYPE: PRT
ORGANISM: Homo sapian
US-10-455-822-7
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      GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Ge, Mangmao

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Faris, Mary

ITITE OF INVENTION: Entitled 98P4B6 Useful in Treatmen

FILE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assig:
PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: US/60/370,387

PRIOR FILING DATE: 2002-04-05
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Sequence 19, Application US/10455822 Publication No. US20040048798A1

nding Proteins Treatment and

Detection of

Cancer

Assigned

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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR PELING DATE: 2001-06-06
PRIOR PELING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 198-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR PILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOPTWARE: RastSEQ for Windows Version 4.0
SEQ ID NO
SEQ ID NO
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                 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
                                                            1SFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                                                                  CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
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; PRIOR APPLICATION NUMBER: US60/317,840
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US60/296,656
; PRIOR APPLICATION NUMBER: US60/091,183
; PRIOR FILING DATE: 1098-06-30
; PRIOR PILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US60/087,520
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NUMBER: US60/087,520
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; SEQ ID NO 19
; LENGTH: 454
; TYPE: PAT
; ORGANISM: Homo sapian
US-10-455-822-19
                                                                                                                                                                      Sequence 21, Application US/10455822
Publication No. US20040048798A1
GENERAL INFORMATION:
APPLICANT: Agensys Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
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APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Pro
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatmer
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION UNMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: No.
PRIOR APPLICATION NUMBER: 0520040048798A1 Yet Assig
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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US-10-455-822-21
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RESULT 7 US-10-455-822-23 ; Sequence 23, Application US/10455822 ; Publication No. US20040048798A1

GENERAL INFORMATION:

APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia
APPLICANT: Faris, Mary

Pia M.

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APPLICANT: Faris, Mary

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and

FILE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/01/455,822

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR FILING DATE: 2002-04-05

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; TYPE: PRT; ORGANISM: Homo US-10-455-822-21
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 21
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Best Local Similarity 100
Matches 454; Conservative
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
                  EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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                                                       ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapian
US-10-455-822-23
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and Det
FILE REFERENCE: 51158-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/00-12-20
PRIOR APPLICATION NUMBER: US/00-370,387
PRIOR FILING DATE: 2002-04-05
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US-10-455-822-25
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Best Local Simi
Matches 454;
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                                                                                                                                                                                                                               APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
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No. US20040048798A1
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Pred. No. 6.1e-222;
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      GENERAL INFORMATION:

APPLICANT: Agensys, Inc.

APPLICANT: Raitano, Arthur B.

APPLICANT: Raitano, Arthur B.

APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Paris, Mary

ITILE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and Det

FILE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned

PRIOR FILING DATE: 2002-10-20

PRIOR APPLICATION NUMBER: US/60/370,387

PRIOR APPLICATION NUMBER: US/60/370,387
                                                                                                                                                                                                                                                                                                                                RESULT 9 10-455-822-31 US-10-455-822-31, Application US/10455822 Sequence 31, Application US/10455822 Publication No. US20040048798A1
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER: OF SEQ ID NOS: 197
SOFTWARE: FABLISEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapian
US-10-455-822-25
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Best Local Similarity
Matches 454; Conserv
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                              EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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SEQ ID NO 31

LENGTH: 454

TYPE: PRT

ORGANISM: Homo sapian

US-10-455-822-31
                                                                                                                                                                                                               Sequence 33, Application US/104, Publication No. US20040048798A; GENERAL INFORMATION:
APPLICANT: Agensys, Inc., APPLICANT: Raitano, Arthur B, APPLICANT: Ge, Mangmao
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APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Pro
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment Reperson 151158-20016-24
CURRENT APPLICATION UNMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO.
PRIOR APPLICATION NUMBER: NO.
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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US-10-455-822-33
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OR FILING DATE: 2001-09-06
OR APPLICATION NUMBER: US60/296,656
OR APPLICATION NUMBER: US60/091,183
OR FILING DATE: 1998-06-30
OR APPLICATION NUMBER: US60/087,520
OR FILING DATE: 1998-06-01
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DR FILING DATE: 1998-06-01
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No. US20040048798A1
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Conservative 0
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Pred. No. 6.1e-222;
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     APPLICANT: Agensys, Inc.
APPLICANT: Raitean, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovits, Aya
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Moleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treatment and Det
FILE REFERENCE: 51158-20016.34
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: NO. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US/00/370,387
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR RIFLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER: OF SEQ ID NOS: 197
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 454
TYPE: PAT
ORGANISM: Homo sapian
US-10-455-822-33
                                                             RESULT 11
US-10-455-822-35
Sequence 35, Application US/10455822 Publication No. US20040048798A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 454; Conserv
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Pred. No. 6.1e-222;
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US-10-455-822-35
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
PRIOR FILING DATE: 1998-06-01
NUMBER: OF SEQ ID NOS: 197
NUMBER: OF SEQ ID NOS: 197
                                                                                                                                                                       APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovite, Aya
APPLICANT: Challita-Bid, Pia M
APPLICANT: Faris, Mary
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LENGTH: 454
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Best Local Similarity
Matches 454; Conserv
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                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/10455822 Publication No. US20040048798A1
                APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding
TITLE OF INVENTION: Entitled 98P4B6 Useful in Treat
FILE REFERENCE: 511.88-20016.24
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet As
PRIOR FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US60/370,387
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FILING DATE: 2002-04-05
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Publication No. US20040048798A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raitano, Arthur B.
                TITLE OF INVENTION: Nucleic acids and Corresponding Prote TITLE OF INVENTION: Entitled 989486 (Useful in Treatment FILE REFERENCE: 51189-20016.24 CURRENT APPLICATION NUMBER: US/10/455,822 CURRENT FILING DATE: 2003-06-04 PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigne PRIOR FILING DATE: 2002-12-20 PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigne PRIOR FILING DATE: 2002-12-20 PRIOR APPLICATION NUMBER: WS60/370,387
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APPLICANT:
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Jakobovits, Aya
Challita-Eid, Pi
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vo. US20040048798A1
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; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 37
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapian
US-10-455-822-37
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PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
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Best Local Similarity
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                                 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454
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EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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100.0%; Pred. No. 6.1e-222;
tive 0; Mismatches 0;
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APPLICANT: Ge, Wangmao

APPLICANT: Jakobovits, Aya

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Challita-Eid, Pia M.

APPLICANT: Faris, Mary

TITLE OF INVENTION: Nucleic acids and Corresponding Proteins

TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and Det

FILE REFERENCE: 51158-20016.24

FILE REFERENCE: 51158-20016.24

CURRENT APPLICATION NUMBER: US/10/455,822

CURRENT FILING DATE: 2003-06-04

PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned

PRIOR APPLICATION NUMBER: US60/370,387

PRIOR FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2001-09-06
PRIOR PELICATION NUMBER: US60/296,656
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR PILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-01
NUMBER OF SBQ 1D NOS: 197
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 454
TYPE: PRT
ORGANISM: Homo Sapian
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US-10-455-822-78
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Best Local S
Matches 454
                                                                                                                                                                                                                                                           Sequence 78, Application US/1045822
Publication No. US20040048798A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Raiteno, Arthur B.
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  GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Agensys, Inc.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Faris, Mary
TITLE OF INVENTION: Nucleic acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 98P486 Useful in Treatment and Det
TILE OF INVENTION NUMBER: US/10/455,822
CURRENT APPLICATION NUMBER: US/10/455,822
CURRENT FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: No. US20040048798A1 Yet Assigned
PRIOR APPLICATION NUMBER: US60/370,387
PRIOR FILING DATE: 2002-04-05
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Application US/10455822 10. US20040048798A1

Detection

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PRIOR APPLICATION NUMBER: US60/317,840
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: US60/296,656
PRIOR APPLICATION NUMBER: US60/091,183
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR APPLICATION NUMBER: US60/087,520
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 454
TYPE: PAT
ORGANISM: Homo Sapian
US-10-455-822-78
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Best Local Similarity 100.0%; P
Matches 454; Conservative 0;
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Pred. No. 6.1e-222;
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; PRIOR APPLICATION NUMBER: US60/317,840
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US60/296,656
; PRIOR APPLICATION NUMBER: US60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR FILING DATE: 1998-06-01
; PRIOR FILING DATE: 1998-06-01
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FSEUSEQ for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapian
US-10-455-822-121
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Search completed: April 16, 2004, 12:46:36
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-655-166A-879
US-09-655-270A-15
US-09-655-291-17
US-09-655-991-17
US-08-487-886-2
US-08-487-886-2
US-08-487-886-2
US-08-487-886-2
US-09-323-873A-2
US-09-333-973A-2
US-09-333-70A-3
US-09-333-70A-3
US-09-316-083-3
US-09-170-496D-226
US-09-170-496D-226
US-09-364-425B-27
US-08-75-74-974A-2
US-08-75-73-42D-6
US-09-975-413A-10
US-09-975-413A-10
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Sequence 1, Appli
Sequence 2, Appli
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appli
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Sequence 3, Appli
Sequence 3, Appli
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Sequence 118, Appli
Sequence 11944, A
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Sequence 6, Appli
Sequence 61, Appl
Sequence 10, Appl
Sequence 6009, Appl
Sequence 2922, Ap
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94 4.0 292 4 US-09-903-456-83 94 4.0 293 4 US-09-903-456-85 94 4.0 293 4 US-09-903-456-85 94 4.0 293 4 US-09-903-456-45 93 4.0 365 2 US-08-724-974A-3 93 4.0 498 4 US-09-107-532A-7077 92.5 3.9 405 4 US-09-489-039A-9411 91.5 3.9 405 4 US-09-489-332-5605 91.5 3.9 497 4 US-09-252-991A-23822 91 3.9 410 4 US-09-252-991A-23822 91 3.9 550 4 US-09-634-288-281 91 3.9 550 4 US-09-634-288-281 91 3.9 550 4 US-09-634-288-281 91 3.9 550 4 US-09-134-001C-3105 90.5 3.8 388 4 US-09-178-032B-26 90.5 3.8 388 4 US-09-178-033B-26 90 3.8 500 4 US-09-178-033B-26 90 3.8 495 1 US-09-795-927-7 89.5 3.8 495 1 US-08-290-301-2	45	44	43	42	41	40	39	38	37	36	35	34	υ G	32	3 ⊥	30	29	28
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## ALIGNMENTS

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APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREF
FILE REPERNCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/081,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Daniel E. Hubert
APPLICANT: Kahan Leong
APPLICANT: Kahan Leong
APPLICANT: Arthur B. Raitan
APPLICANT: Douglas C. Saffr.
APPLICANT: Steve Chappell M
                                                                                                                                                                                                                                                                                                                                            ; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-323-873A-8
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Best Local Similarity
Matches 173; Conserv
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                                          366
                                                                                                                              306
                                                                                                                                                                                                      246 DFYKIPIBIVNKTLPIVAITLLSLVYLAGILAAAYQLYYGTKYRRFPPWLETWLQCRKQL
  121
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MSLGLISILAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRA 173
                            MSLGILSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKKA 418
                                                                                                                    GLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGI
                                                                                                                                                                        dfykipibivnktlpivaitllslvylagllaaayqlyygtkykkfppwlbtwlqckkql
                                                                                      GLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGI
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                                                                                                                                                                                                                                                                                                         Length 173;
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RESULT 2 US-09-083-521-1

Sequence 1, Application US/09083521
Patent No. 6048970
GENERAL INFORMATION:

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; LIBRARY: PROSTUT10
; CLONE: 1691243
US-09-083-521-1
                                                                                                                                                                                                                                                                                    US-09-323-873A-2
                                                                                                                                                                               Sequence 2, Application US/09323873A
PALENT NO. 6329503
GENERAL INFORMATION:
APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 141;
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LENGTH: 141 amino acids
          APPLICANT: Arthur B. Raitano
APPLICANT: Douglas C. Saffran
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THE
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT FILING DATE: 1999-06-01
                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
RITLE OF INVENTION: PROSTATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CERRONE, MICHAEL C.
RECIFICATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 31.3%; Score 736; DB 3; Le Local Similarity 100.0%; Pred. No. 2.2e-69; O; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 LAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEBEYYRFYTPPNFV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 WYHVAYSLCLPMRRSERYLFLNWAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSL
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                                                                                                                                                                    Kahan Leong
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NUMBER:
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                                                                                                                      ; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-685-166A-879
                                                                                                                                                                                APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: 210121.427C21
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
SEQ ID NO 879
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Best Local
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PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version
                                                   Query Match
Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 339
TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 WREFSFIOSTIGYVALLISTFHVLIYGWKKAFEEEXYRFYTPENFVLALVLPSIVIL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 SLYYLAGLLAAAYQLYYGTKYRREPPWLETWLQCRKQLGLLSFFFAMVHVAYSLCLPWRR 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 LETLWRGPVVVAISLATEFELYSFVRDVIHPYARNQQSDEYKIPIEIVNKTLPIVAITLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 30.5%; Score 717; DB 4; Similarity 54.9%; Pred. No. 8.5e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Fanger, Gary R. Retter, Marc W. Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalos, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                  Vedvick, Thomas
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jiang, Yuqui
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Craig H.
                                                                                                                                                                                                                                                                                                                                                                                                                  Thomas S.
                                                                       30.5%;
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                                                      Score 717; DB 4;
Pred. No. 8.5e-67;
B; Mismatches 59;
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RESULT 5
US-09-655-270A-15
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NUMBER OF SEQ ID NOS:
SOFTWARE: Microsoft Of
SEQ ID NO 15
LENGTH: 227
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APPLICANT: ROUVIER, PIERRE E
APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DANA M
APPLICANT: RAINER, RUSS
TITLE OF INVENTION: Genes Encoding Picric Ac:
FILE REFERENCE: BC1022 US NA
CURRENT APPLICATION UNMEER: US/09/651,941
CURRENT FILING DATE: 2000-08-31
CURRENT FILING DATE: 1999-10-03
PRICR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                            Sequence 17, Application US/09651941 Patent No. 6355470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: High Density Sampling
FILE REFERENCE: BC1011 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Rhodococcus erythropolis HL PM-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; Score 144.5; DB 4; Similarity 28.0%; Pred. No. 6.4e-07; 60; Conservative 33; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKSSKIAVVG--GTGPQGKGLAYRFAAAGWPVVIGSRSAERAEEAALEVRRRAGDGAVVS 58
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APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DANA M
APPLICANT: WALTERS, DONA
FILLE OF INVENTION: Genes Encoding Picric Acid December of the Control of the Current APPLICATION NUMBER: US/09/955,597
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/152,545
PRIOR FILING DATE: 1999-10-03
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 227
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TYPE: PRT
CRGANISM: Rhodococcus erythropolis HL
US-09-651-941-17
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; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-955-997-17
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US-09-955-597-17
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            RESULT 8
US-08-487-886-2
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Patent No. 646185
GENERAL INFORMATI
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SEQ ID NO 17
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Best Local
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Best Local Similarity
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                                                                                                      LAVAITGRPGIDGGALRVARQLEPLTAVLINVNR
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density

COMPUTER: IBM PS/2, model 55 SX

OPERATING SYSTEM: MS-DOS version 4.0

SOFTWARE: VAX/VMS MASSI1 via Kermit to IBM MS-DOS

CURRENT APPLICATION NUMBER: US/08/487,886

FILING DATE: 07-JUN-1995

CLASSIFICATION NUMBER: 07/670,085

FILING DATE: 15-MAR-1991

APPLICATION NUMBER: 28546

REGISTRATION NUMBER: 28546

REGISTRATION NUMBER: 28546

REFERENCE/DOCKET NUMBER: US/252

TELECOMMUNICATION INFORMATION:

NAME: Williams, Stephan P.

REGISTRATION NUMBER: 28546

REFERENCE/DOCKET NUMBER: US/252

TELECOMONICATION INFORMATION:

TELEPAX: (617) 723-830

TELEPHONE: (617) 723-8923

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 695
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NAME/KEY: signal sequence

LOCATION: -17 to -1

IDENTIFICATION METHOD: hydrophobic
FEATURE:
NAME/KEY:
LOCATION:
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APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 5744448een Patrice
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NAME/KEY: transmembrane
LOCATION: 350 to 613
IDENTIFICATION METHOD: E
IDENTIFICATION METHOD: F
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NAME/KEY:
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ZIP: 021
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ADDRESSEE: Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: putative amino-terminal extracellular LOCATION: 1 to 349
IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receptantification METHOD: domains, hydrophilic
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TOPOLOGY:
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                                                                           LOCATION: 382 to 404 IDENTIFICATION METHOD: IDENTIFICATION METHOD: IDENTIFICATION METHOD:
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  putative transmembrane region III 427 to 448
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putative transmembrane region IV 469 to 491 TION METHOD: similarity to other similarity to other G protein-coupled receptor hydrophobic, about 20-23 transmembrane regions amino acids in length transmembrane amino acids in regions, n length

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Length

Indels 185;

Gaps

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RSTYNLKKLP----TIEKLVALMEASITYPSHCCAFANWRRQISELHPICNKSILRQE NQQSDFYKIPIEIVKTL-PIVAITLLSLVY-------

300

271

VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTBFDYDLCNEVVDVTCSPKPDAFNPCEDIM 360 305

SVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVV/GWIFAFAAALFPIFGISSYMKVS GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVP----RFLMCNLAFAD-----SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWRE-----FSFIQSTL -----LCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASEL ----YSLCLPMRRSERYLFLNMAYQQVHANIEN 347 ----VLIYGWKRAFEEEYYRFYTPPNFV-LA

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RESULT 9
US-08-482-855-2
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Patent No.
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INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 695

TYPE
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APPLICANT:
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MEDIUM TYPE: 3.5" diskette, 1.44 MB,

COMPUTER: IBM PS/2, model 55 SX

COMPUTER: IBM PS/2, model 55 SX

COMPUTER: MS-DOS version 4.0
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/482,855
PTITMS PAGE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
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LOCATION:
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STREET: Exchange Place, 37th floor
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: putative amino-terminal extracellular LOCATION: 1 to 349
IDENTIFICATION METHOD: similarity with other IDENTIFICATION METHOD: dimeric glycoprotein receDENTIFICATION METHOD: domains, hydrophilic
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NAME/KEY: putative transmembrane region LOCATION: 382 to 404 LOCATION SIMILARITY to oth IDENTIFICATION METHOD: protein-coupled rIDENTIFICATION METHOD: hydrophobic, about
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LICANT: Nugent, No. 6121016een Patrice
LE OF INVENTION: Human Follicle Stimulating
LE OF INVENTION: Hormone Recentor
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SVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGISSYMKVS
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17.0%; Pred. No. 0.028;
ative 77; Mismatches 1
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                                                                                                                 VLIYGWKRAFEEEYYRFYTPPNFV-LA
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TELEFAX: (617) 723-8923

LOCATION: 614 to 678

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-08-474-986-2
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US-08-474-986-2
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Matches 84
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APPLICANT: Kelton, Christie Ann
Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 637271leen Patrice
NUGENTION: Human Follicle Stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 4.6%; Score 107.5; DB 4; Length 695;
Local Similarity 17.0%; Pred. No. 0.028;
hes 84; Conservative 77; Mismatches 148; Indels 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density

COMPUTER: 1BM 98/2, model 55 SX

COMPUTER: 1BM 98/2, model 55 SX

OPERATING SYSTEM: MS-DOS version 4.0

SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
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CORRESPONDENCE ADDRESS: Stephan P. Williams,
ADDRESSEE: Stephan P. Williams,
Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: <Unknown>
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                                      306 G----LLSFFFAMVHVA---------YSLCLPMRRSERYLFLNMAYQQVHANIEN 347
                                                                                    301 VDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFDYDLCNEVVDVTCSFKPDAFNPCEDIM
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STATE: MA
COUNTRY: USA
  GYNILRVLIWFISILAITGNIIVLVILTTSQYKLTVP----RFLMCNLAFAD-----
                                                                                                                                  Hormone Receptor
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Query Match 4.4%; Score 102.5; DB 4; Length 940; Best Local Similarity 19.5%; Pred. No. 0.15; Matches 71; Conservative 74; Mismatches 146; Indels 73; Gaps 17;	WS-09-328-352-8165 ; Sequence 8165, Application US/09328352 ; Patent No. 6562958 ; GENERAL INFORMATION: APPLICANT: Gary L. Breton et al. APPLICANT: Gary L. Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER; TILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/328,352 ; CURRENT FILING DATE: 1999-06-04 ; NUMBER OF SEQ ID NOS: 8252 ; SEQ ID NO 8165 LENGTH: 940 ; TYPE: PRT CORGANISM: Acinetobacter baumannii US-09-328-352-8165	Query Match 4.6%; Score 107; DB 4; Length 34; Best Local Similarity 58.8%; Pred. No. 0.0003; Matches 20; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  y 326 RRSERYLFLNMAYQQVHANIENSWNEEEVWRIEM 359	US-09-323-873A-20  US-09-323-873A-20  Sequence 20, Application US/09323873A  Patent No. 6329503  GENERAL INFORMATION:  APPLICANT: Benies E. Hubert  APPLICANT: Benies E. Hubert  APPLICANT: Arthur B. Raitano  APPLICANT: Arthur B. Raitano  APPLICANT: Steve Chappell Mitchell  APPLICANT: Steve Chappell Mitchell  TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS  TITLE OF INVENTION: NOVEL SERENTINE TRANSMEMBRANE ANTIGENS  TITLE OF INVENTION NOVEL SERENTINE TRANSMEMBRANE ANTIGENS  TILE REFERENCE: 129 16USU2  CURRENT PILING DATE: 1990-06-01  PRIOR APPLICATION NUMBER: 60/091,520  PRIOR APPLICATION NUMBER: 60/091,520  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATION NUMBER: 60/091,183  PRIOR APPLICATI	436 LVLPSIVILDLLQL 449 	399 GYVALLISTEHVLIYGWKRAFEBEYYREYTPENEV-LA 435	348 SWNEEEVWRIEMYISFGIMSLGLLSLLAVTSIPSVSNALNWREF8FIQSTL 398  1

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RESULT 13
US-09-316-083-3
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Patent No. 6280942
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SEQ ID NO 3
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APPLICANT: The Inst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/316,083A CURRENT FILING DATE: 1999-05-20 EARLIER APPLICATION NUMBER: JP98/141861 EARLIER FILING DATE: 1998-05-22 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: The Institute of Physical TITLE OF INVENTION: Endonuclease FILE REFERENCE: PH-651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 476
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452
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                                                                                                                                                                                                                                                                                  254 NPYFVNAFSINI------KTNLAKEKIFTNIYNKLYSDYKINQINNHIPYYNYLK 302
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                                                                                                                                                                                                                                                                                                                                                                     h 4.3%; Score 101; DB 3; Length 476; Similarity 20.7%; Pred. No. 0.075;
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 DNYDYYYYNKY 462
                                 AAYQLYYGTKY 288
                                                                                                     LATEFFLYSFVRDVIHFYARNOOSDFYKIP----IBIVNKTLPIVAITLLSLVYLAGLLA
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                                                                     --FIYYF--DKFLPLHDNKQFNYIKFRFNTFIKSYNWNNRVFGLVLSE--YINNIKI 451
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RESULT 14
US-09-933-700-3
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US-09-252-991A-21494
Query Match
Best Local Similarity
Thes 72; Conserve
                                                                                                                                                                              ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21494
                                                                                                                                                                                                                                                                       APPLICATION UNUBER: US 60/094,190
PRIOR PILLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21494
LENGTH: 724
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Best Local S
Matches 52
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LENGTH: 476
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                        TYPE: PRT
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                               4.3%; Score 101; DB larity 20.5%; Pred. No. 0.14; Conservative 57; Mismatches
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80;	565 TDTAIQHSLGLGGKSRPNTRALIMLPLIRNVLFATIAVIALIVA 608	Db 5	-
406	367SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLIS	Qy 3	~
WLIWIL 564	516 FVVLFFIEVALRVWGMSLIR-YAEGEGEQISMKVVSFGTTLLVAWLIWIL 564	Db 5	-
366	318 AYSICLPMRRSERYLFLNMAYQQVHANIENSWNEBEVWRIEM-YISFGIM 366	Оу з	_
утьтні 215	472 VLAVVAMTVIGLIRRRSSRVGAGPRRSAPYIBQLQSFGYTLLHI 515	Db 4	-
SFFFAMVHV 317	258 TLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFBPWLETWLQCRKQLGLLSFFFAMVHV 317	Ωу 2	$\sim$
RALVCA 471	412 LIRNOPLERRLKRRSLHDLVQLVGSLWFVPVLVLVGISLFATFVSAGDSSSALRRALVCA 471	Db 4	-
-EIVNK 257	239 YARNQQEIVNK 257	0у 2	•
RPIAH- 411	353 FRÞÍMLIGSLAALGEVAHDÞRLIAGLGEHTSICLSTLÁNASAALFTALFVMRFRRÞIAH- 411	Db. 3	-
RDVIHP 238	187 FIPIDL-GSLSSAREIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHP 238	0у 1	_
ILRROA 352	298 YLSVVLPDSL-SKTLAMVMAYVLVCGTLFSALCVISLSLLSGPHRQRALDILRRQA 352	Db 2	-
LARQLN 186	132 YLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIELARQLN 186	0у 1	•

Search completed: April 16, 2004, 12:41:47 Job time : 24 secs

Run on:

OM protein - protein search, using sw

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Result
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Listing first 45 summaries
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Human six transmembrane epithelial antigen of prostate (STEAP)-2 protein. Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-2; STEAP-2; chromosome 7q21; cancer; prostate; colon; bladder; lung; ovarian; label= HLA-A2\_binding\_peptide #5 abel= Transmembrane\_domain #2 .abel= Immunogenic\_peptide #1 Transmembrane\_domain #3 HLA-A2\_binding\_peptide #1 Transmembrane\_domain #1

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                                                                              ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
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     EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
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Pred. No. 5e-245;
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AAU10188; AAU10188 standard; protein; 454

16-JAN-2002

(first

entry)

Human; Six-Transmembrane Protein of Prostate 1; STMP1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer; Human ORF2 cancer; lung cancer; cytostatic; ORF2 of Six-Transmembrane Protein of Prostate

WC200172962-A2

04-OCT-2001

23-MAR-2001; 2001WO-US009410.

24-MAR-2000; 2000US-0191929P

(SAAT/) SAATCIOGLU F.

'FJ

WPI; 2001-662926/76. N-PSDB; AAS15810, AAS15811.

New polynucleotide for the diagnosis, prevention and treatment prostate and testis disorders, particularly prostate cancer, coprostate-specific or testis-specific nucleic acids. comprises

Claim 1; Fig 4H; 114pp; English.

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AXX IIvv The invention relates to substantially pure prostate-specific or testiscolor specific polypeptides and the nucleic acids encoding them. Also included are vectors and host cells expressing the proteins, a transgenic animal expressing the protein, antibodies against the proteins, probes for cexpressing the nucleic acids, antisense molecules for the nucleic acids and methods of isolating modulators of the proteins. Compounds that commodulate the prostate specific or testis specific polypeptide are useful to diagnose, prevent or treat disorders of the testis or prostate (C particularly prostate cancer, benign prostatic hyperplasia, acute prostatitis, testicular cancer, cryptorchidism, undescended, retractile, ascending or vanished testis. Other proliferative disorders for which the cancer, breast cancer, pancreatic cancer, breast cancer, pancreatic cancer, breast cancer, pancreatic cancer, pancreatic cancer, standard and cancer. The present sequence is prostate specific protein, Six-Transmembrane or protein of Prostate 1, STMP1, ORF2

Sequence 454 Ã

Length

밁 Ś 片 ş Query Match Best Local S 454; 61 61 Similarity RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESIGNMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDPAKSLTIRLIRCGYHVVIGS MESISMMGS PKSLSETCLPNGINGIKDARKVTVGV 100.0%; ilarity 100.0%; Conservative VTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM 0 Score 2351; DB 4; Pred. No. 5e-245; IGSGDFAKSLTIRLIRCGYHVVIGS Indels 0 Gaps 120 60 60

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08-DEC-2000; 2000US-00733288.
08-DEC-2000; 2000US-00733742.
24-JAN-2001; 2001US-0263957P.
16-MAR-2001; 2001US-0276791P.
16-MAR-2001; 2001US-0276888P.
06-APR-2001; 2001US-0281922P.
24-APR-2001; 2001US-028214P.
30-APR-2001; 2001US-0288589P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L933
                                                                        Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                         18-APR-2002
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The present invention relates to methods of detecting a prostate cancer-
associated transcript in a cell from a patient. The method comprises
contacting a biological sample from the patient with prostate cancer-
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                                              Claim
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)B; ABK92252.
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                                             27; Page 416; 436pp;
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Matches 454;
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                        EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD
                                                            ISFGINSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTEHVLIYGWKRAFE
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The invention relates to an isolated tumour-associated antigenic target CC polypueptide (TAT) (I), specifically TAT138 polypeptides, and the CC polypucleotides (II) encoding them. (II) is useful for diagnosing the CC presence of a tumour in a mammal, where the level of expression of (II) is indicative on the presence of tumour in the mammal from which the test CC sample was obtained. Antibody to (I) is useful for killing a cancer cell. (e.g. breast cancer cell, a contral nervous system (CNS) cancer cell, a no varian cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral cancer cell, a pancreatic cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous system (CNS) cancer cell, a contral nervous cancer cell, a contral cancer cell, a contral cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a contral nervous cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a cancer cell, a
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26-SEP-2000; 2000US-0235451P
01-DEC-2000; 2000WO-US032678
28-FEB-2001; 2001WO-US006520
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 Devaux B,
                                                                                                                                                WO200226822-A2
                                                                                                                                                                                                                   Human; protein upregulated in metastatic prostate cancer; immunogen; PUMPCn; PRO23203; prostate cancer; cytostatic; gene therapy; transgenic;
                                                                                                                                                                                                                                                                 Human PUMPCn protein,
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Eberhard D,
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Pred. No. 5e-245
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 Godowski PJ,
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ancer (PUMPCN) PRO23203 polypeptide, a sequence 80%
and the sequence as encoded by cDNA insert of the
TCC Deposit No. PTA-2513 (DNA185171- 2994) on
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Pred. No. 5e-245;
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02-MAR-2000;
30-MAR-2000;
24-AUG-2000;
The invention discloses human nucleic acids encoding tumour-associated antigenic target (TAT) polypeptides, with our without their associated signal peptide. Also disclosed is an antibody that specifically binds to the TAT polypeptides, a method for detecting the presence of a tumour in a mammal and a method for killing a cancer cell expressing the TAT polypeptide. The nucleotide sequences are useful in preparing TAT polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The TAT polypeptides are useful as therapy ending the presence, prevention and/or treatment of a tumour, such as colon, breast or prostate tumour. The TAT polypeptides and nucleic acids may also be used diagnostically for tissue
                                                                                                                                                                                                                                              Goddard .
Wood WI,
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herapy; cytostatic; tissue typing; prostate tumour; cancer.
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2000WO-US032678.
2001WO-US006520.
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Isogai T, Sugiyama T,
Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                28-MAR-2002; 2002EP-00007401
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; tumour.
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25-JAN-2002;
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2002US-00350978.
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     Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
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Pred. No. 5e-245;
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Sequence 454 AA;

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The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel cor its partial peptide, an antibody binding to the polypuptide or peptide of the polynucleotide, immunologically assaying the polypuptide or peptide of the polynucleotide by contacting the polypuptide or peptide cor with the antibody of the encoded protein, and observing the binding contacting the polynucleotide between the two, a transformant carrying the polynucleotide is useful as a primer for synthesising the polynucleotide, or as a probe for detecting the polynucleotide. The oligonucleotide cor sections are useful as pharmaceutical agents and many disease-related cor genes may be included in them, for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy. The genes are involved in tissue and/or cell concoding them can be used as indicators for developing a diagnostic marker or transcription-related proteins, disease-related proteins and genes are involved in tissue and/or cell the activity or expression of the encoded proteins and genes are the activity or expression of the encoded protein and genes are the activity or expression of the encoded protein to treat diseases. The sequence presented is a protein of the invention. Note: Some of the securion particle is based on sequence information supplied by the conception patent office.
XEEXEFEXXXXOOOOOOOOOOOOOOOOOOOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.
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N-PSDB; ADB63031.
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밁 S Ś Ъ Ś 맑 5 g Š 밁 Ş В δ δ В Query Match Best Local Simi Matches 453; 241 181 361 361 301 301 241 181 121 421 421 121 61 61  $\vdash$ Similarity MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM LARQLNFIPIDLGSLSSAREIENLPLRLFTLWRGPVVVAISLATEFFLYSFVRDVIHPYA RINQYDESNAEYLASIFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE | ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNBEEVWRIEMY CRKQLGILSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY EBYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD 454 EEYYRFYTPPNFVLALVLPSIVILDLLQLCRYPD ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE LARQLNFIPIDLGSLSSARBIENLPLRLFTLWRGPVVVAMSLATFFFLYSFVRDVIHPYA Conservative 99.9%; Score 2348; DB 7; Pred. No. 1.1e-244; 1; Mismatches 0; 454 Length 454; Indels °, 240 180 180 120 60 360 300 300 240 120 420 360 420

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Best Local
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                                                                                                                                                                                                                                                                                          Sequence
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ilarity 100.0%;
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The invention relates to a purified human protein comprising a copypeptide having a fully defined transmembrane protein differentially compressed in prostate and lung tumour (TMPL) sequence. The protein is cueful for detecting expression of the protein in a sample, where the compressed in prostate tissue sample and the protein is diagnostic differentially expressed when compared with a standard and is diagnostic of a lung or prostate cancer. The protein is useful to identify an compared with a standard and is diagnostic of a lung or prostate cancer. The protein is useful to identify an compared with a standard and is diagnostic of a lung or prostate cancer. The protein is useful for greening several molecules and compounds to identify at least one compared with a standard and protein is also useful for preparing and purifying a compound to identify at least one compared with a standard animal immunisation/hybridoma methods. A TMPL specific antibody using compounds to detect expression of the protein in a lung or prostate cancer. A TMPL specific antibody is useful as a diagnostic for lung or constate cancer. A TMPL specific antibody is useful for protein a protein, for treating a prostate cancer and for compountifying a protein, for treating a prostate cancer and for the protein is useful for diagnosing, staging, treating or monitoring compounds to the protein of the human of the protein of the protein of the human and the protein of cancer, preferably lung or prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                            Human; Six-Transmembrane Protein of Prostate 1; STM; 1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                            Domain
                                                                                                                                                                        Domain
                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Six-Transmembrane Protein of Prostate 1, STMP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU10187 standard; protein; 490 AA.
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                                                                                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEYYRFYTPPNFVLALVLPSIVIL 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRKQLGLLSFFFAWVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNBEEVWRIEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEYYRFYTPPNFVLALVLPSIVIL 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          lung cancer; cytostatic.
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                            label=
                                                                                                   label=
                                                                                                                                                                                               label=
                                                 .abel=
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  Transmembrane_domain_
                                                                                                                                        Transmembrane_domain_3
                                                                                                                                                                                             Transmembrane_domain_
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                                            Transmembrane_domain_5
                                                                                              Transmembrane_domain_4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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CC specific polypeptides and the nucleic acids encoding them. Also included
CC are vectors and host cells expressing the proteins, a transgenic animal
CC expressing the protein, antibodies against the proteins, probes for
CC and methods of isolating modulators of the proteins. Compounds that
CC and methods of isolating modulators of the proteins. Compounds that
CC to diagnose, prevent or treat disorders of the testis or prostate
CC postatitis, testicular cancer, benign prostatic polypeptide are useful
CC prostatitis, testicular cancer, cryptorchidism, undescended, retractile,
CC ascending or vanished testis. Other proliferative disorders for which the
CC modulators may be used include lymphoma, leukaemia, melanoma, ovarian
CC cancer, breast cancer, pancreatic cancer, liver cancer and lung cancer.
CC Transmembrane Protein of Prostate 1, STM;1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 490 AA;
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N-PSDB; AAS15793, AAS15801, AAS15802.
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                                                                                                                                                                                                                                            RNOQSOFYKIPIBIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
                                                                                                                                                                                                                                                                              RNQQSDFYKIPIBIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
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EEYYRFYTPPNFVLALVLPSIVIL 444
                                               1SFG1MSLGLLSLLAVTS1PSVSNALNWREFSF1QSTLGYVALL1STFHVL1YGWKRAFE
                                                                                    ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE
                                                                                                                                           CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY
                                                                                                                                                                                          CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIENY
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Pred. No. 2.3e-238;
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                                                                                                                                         Query Match
Best Local Sim
Matches 394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Six-Transmembrane Protein of Prostate 1; STM; 1; prostate cancer; benign prostatic hyperplasia; acute prostatitis; testicular cancer; cryptorchidism; testicular disorder; proliferative disorder; lymphoma; leukaemia; melanoma; ovarian cancer; breast cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORF3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 4K; 114pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2002
                                                                                                                                                                                                                Sequence 419
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DB; AAS15813.
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                                                                                                                                                              Similarity
                                                                                         MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
                                  RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
                                                                      MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Six-Transmembrane Protein of Prostate
                                                                                                                                             Conservative
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99.7%;
   VTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM
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                                                                                                                                             Score 2036; DB 4;
Pred. No. 5.5e-211;
0; Mismatches 1;
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain (C reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed (C genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is cueful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (involving aberrant protein expression or biological activity. The collapse of the protein expression or biological activity. The collapse of the protein expression or biological activity. The collapse of the protein expression or biological activity of mutations in the polypeptide and polynuclectide sequences have applications in the collapse of the protein expression of the protein expression or biological activity.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
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                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 42665; 103pp; English.
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supplement; medical imaging; diagnostic;
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2000US-00649167.
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Matches
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                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                        WO200175067-A2
                                                                                                                                                                                     Human; chromosome
                                                                                                                                                                                                                                                                                     ABG00113 standard; protein;
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                                                                        30-MAR-2001;
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imaging; diagnostic; genetic of
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Pred. No. 6.7e-204;
D; Mismatches 1;
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Sequence 1273

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cc sequences. (I) is useful as hybridisation probes, polymerase chain (cc reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polynucleotides are also used cc and in recombinant production of (II). The polynucleotides are also used cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is complypely to the second of the production of quantitating a polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and is binding partners are useful in medical imaging cf sites expressing (III). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The cc polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodivarsity and to produce other types of data and products dependent on DNA and cand sequences. Abdoull-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this calculation format directly from WIPO at cf ftp.wipo.int/pub/published_pct_sequences.
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Ś 멍 Š B Ş B 8 밁 Ś δ g δ 片 밁 Ş Query Match Best Local S Matches 390 313 193 421 361 373 301 241 253 181 121 133 390; 61 73 Similarity MEGISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMY RNQQSDFYKIPIBIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ RINQYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM MESISMMGSPKSLSETFLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGS EEYYRFYTPPNFVLALVLPSIVILDL RNQQSDFYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ LARQLNFIPIDLGSLSSARBIENLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA RINGYPESNAEYLASLFPDSLIVKGFNVVSAWALQLGPKDASRQVYICSNNIQARQQVIE RNPKFASEFFPHVVDVTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNM EEYYRFYTPPNFVLALVLPSIVILDL ISFGIMSLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFE LARQUNFIPIDLGSLSSARBIBNLPLRLFTLWRGPVVVAISLATFFFLYSFVRDVIHPYA Conservative LSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQ--83.9%; Score 1972.5; Pred. No. 2.3e. 0; Mismatches 0, 463 446 .3e-203; OSTLGYVALLISTFHVLIYGWKRAFE DB 4; Indels Length 55, Gaps 120 132 90 372 300 240 180 192 420 252

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RESULT 14
AAE02841
ID AAE028
XX AAE02
XX AAE02
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                                                     The present sequence is an alternative version of human six transmembrane cepithelial antigen of the prostate (STEAP)-2 protein. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-2 gene is cocated on chromosome 7q21 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreatic) expressing STEAP or inhibiting growth or vaccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or inhibiting growth or stilling cells expressing STEAP, or inhibiting growth or stilling cells expressing STEAP, or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain compositional antibody that specifically binds to STEAP, comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, comprises the vector delivers the single chain monoclonal antibody is expressed intracellularly. Note: This sequence is stated to be the same as that being shown as SEO ID NO:8 (AAEO2781) in figure 9A-9C of the specification. However the present sequence lacks several amino acids at its C-terminal end when compared with the sequence shown in figure 9A-9C terminal end when compared with the sequence shown in figure 9A-9C
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Matches 336;
                                                                                                                           New polynucleotide and polypeptides, useful for treatment and d of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, m sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; vulnerary; dermatological; neuroprotective; nootropic; car
antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
antidiabetic; antiallergic; gene therapy; wound healing; tissue r
burn; central nervous system disorder; Alzheimer's disease;
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                                                                            SEQ ID NO 320; 284pp + Sequence Listing; English
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lu C, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1082 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 MRINQYPESNAEYLASLFPDSLIVKGFNVVSAMALQLGPKDASRQVYICSNNIQARQQVI
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                                                                                                                       420 EEEYYRFYTPPNFVLALVLPSIVILDL 446
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                                                                                               EEEYYRFYTPPNFVLALVLPSIVILDL 272
                                                                                                                                                                                                                                                                                 QCRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQ--------
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